

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:28:11 ; Search time 20004.5 Seconds
(without alignments)
1964.002 Million cell updates/sec

Title: US-09-636-259C-1
Perfect score: 1350
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	1350	100.0	204908	9	AL158163	AL158163 Human DNA
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10	1319	97.7	1521	9	HUMADRA	M18415 Human plate
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13	1106.8	82.0	1552	10	RRU79031	U79031 Rattus norv
14	1095.6	81.2	1380	10	RATRG20	M62372 Rat alpha-2
15	1095	81.1	2923	4	BTU79030	U79030 Bos taurus
16	1084.4	80.3	1454	10	MUSALP2ADB	M99377 Mouse alpha
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ALIGNMENTS

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DEFINITION Sequence 24 from Patent WO0179561.
ACCESSION AX350512
VERSION AX350512.1 GI:18616107
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 24 25-OCT-2001;

FEATURES		Liggett, Stephen B. (US) ; Small, Kersten M. (US)	
source		Location/Qualifiers	
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ACCESSION AF281308			
VERSION AF281308.1 GI:9652209			
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ORGANISM Homo sapiens			
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REFERENCE 1 (bases 1 to 1353)			
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.			
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling			
JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)			
MEDLINE 20556293			
PUBMED 10948191			
REFERENCE 2 (bases 1 to 1353)			
AUTHORS Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.			
TITLE Direct Submission			
JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA			
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RESULT 4					
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DEFINITION	Homo sapiens alpha-2A adrenergic receptor (ADR2AR) gene, complete cds.				
ACCESSION	AY032736				
VERSION	AY032736.1				
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 3612)				
TITLE	Liu, L. and Yuan, L.				
JOURNAL	Human alpha-2A adrenergic receptor gene and the genotype of -1296 nucleotide and motionsickness				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 3612)				
TITLE	Liu, L. and Yuan, L.				
JOURNAL	Direct Submission				
FEATURES	Submitted (17-APR-2001) Key Laboratory of Molecular Biology, General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036, China				
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RESULT 6
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VERSION AL158163.11 GI:17384427
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 204908)
AUTHORS Johnson,C.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Dec 5, 2001 this sequence version replaced gi:16944857.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10> RP11-348N5 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6

This sequence is the entire insert of clone RP11-348N5 The true left end of clone RP11-479A21 is at 179266 in this sequence. The true right end of clone RP11-313D6 is at 44800 in this sequence.

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REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 25 25-OCT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M. (US)
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Db	1258	GTGCTCGTGCCACGACGCTCTTCAAATCTTCTTCTGGTTCGGCTACTGCAACAGCTC 1317
Qy	1260	GTTGAACCCGTCATCTACACCATCTTCAACCCACGATTTCCGCGCGCTTCAAGAAGAT 1319
Db	1318	GTTGAACCCGTCATCTACACCATCTTCAACCCACGATTTCCGCGCGCTTCAAGAAGAT 1377
Qy	1320	CCTCTGTCGGGGGACAGGAAGCGGATCGTG 1350
Db	1378	CCTCTGTCGGGGGACAGGAAGCGGATCGTG 1408

RESULT 11	PIGA2AR	1728 bp	DNA	linear	MAM 27-APR-1993
LOCUS	Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.				
DEFINITION	Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.				
ACCESSION	J05652				
VERSION	J05652.1 GI:164303				
KEYWORDS	alpha-2A-adrenergic receptor.				
SOURCE	Porcine liver DNA.				
ORGANISM	Sus scrofa				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
AUTHORS	1 (bases 1 to 1728) Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Kragoe,E.J.Jr. and Limbird,L.E.				
JOURNAL	Unpublished (1990)				
REFERENCE	2 (bases 70 to 1582) Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Cragoe,E.J. Jr. and Limbird,L.E.				
AUTHORS	Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Na+, H+, and amiloride analogs				
TITLE	J. Biol. Chem. 265 (28), 17307-17317 (1990)				
JOURNAL					
MEDLINE	91009167				
PUBMED	2170371				
COMMENT	Draft entry and computer-readable sequence for [J. Biol. Chem. (1990) In press] kindly submitted by C.A.Guyer, 02-AUG-1990.				
FEATURES	Location/Qualifiers				
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CDS					

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/translation="MGSLOPEAGNASWNGTEAPGGARATPYSLQVTLTLVCLAGLLM									
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KAWCEIYLALDVLFPCTSSIVHLCAISLDRYWSITQAIENLKRTPRRIKAIIVTWVI									
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IVQIAKRTRTRVPSRRGPDAAAALPGGAERRPNGLGPRGVGAEAEPLVPQLNGA									
PGEAPAGPRDADGLDLEESSSEHAERPGRRSERGPRAKSKARASOVKPGDSLPR									
RPGAPGPGAPATGAGEERGVAKASRWGRQNRKRTFTFLAVVIGVFWVCWFFPFF									
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BASE COUNT 268 a 590 c 562 g 308 t									
ORIGIN									
Query Match 85.2%; Score 1150; DB 4; Length 1728;									
Best Local Similarity 90.7%; Pred. No. 1.8e-134;									
Matches 1225; Conservative 0; Mismatches 125; Indels 0; Gaps 0;									
QY	1	ATGGGCTCCTG	CAGCCGGAC	CGGGCAAC	CGGAGCTG	GAAACGGG	ACCGGAC	CGGCGCCGGG	60
Db	130	ATGGGCTCCTG	CAGCCGGAA	CGGGCAAC	CGGAGCTG	GGAATGGG	ACAGAGG	CGCGCCGGG	189
QY	61	GGCGGCGCCG	GGGCCAC	CCCTTACT	CCCTGC	AGGTGAC	CGTGAC	CGTGGCTGGCC	120
Db	190	GGCGGCGCCG	GGGCCAC	CCCCCTACT	CCCTGC	AGGTGAC	ACTGAC	GTGGTGTGCC	249
QY	121	GGCCTGCTCAT	GTGCTCAC	CGTGTT	CGGSAAC	GTGCTCGT	CTCAT	ATCGCCGTTCACG	180
Db	250	GGCCTGCTCAT	GTGTTAC	CGGTGTT	CGGSAAC	GTGCTTGTCAT	CATTGCCGTGTT	TCACA 309	
QY	181	AGCCGCGCGCT	CAAGGCGCC	CCCAAA	CCCTTCT	CCTGGT	GTCTCG	GCCTCGGCCGACATC 240	
Db	310	AGCCGCGCGCT	CAAGGCGCC	CCCAAA	CCCTTCT	CCTGGT	GTCTCG	GCCTCGGCCGACATC 369	
QY	241	CTGGTGGCCAC	GGTCGT	CATCCCTTT	CTCGTGG	CAACGAG	GTGATGG	GCTACTGGTAC 300	
Db	370	CTAGTGGCCAC	GGTTGT	CATCCCTTT	CTCGTGG	CAACGAG	GTGATGG	GCTACTGGTAC 429	
QY	301	TTCGGCAAGG	CTTGGT	CGGAGATCTA	CTGGCG	CTCGAC	GTCTTCTG	CACGTCTGCC 360	
Db	430	TTCGGCAAGG	CTTGGT	GTGAGATCTA	CTGGCG	CTCGAC	GTCTTCTG	CACGTCTGCC 489	
QY	361	ATCGTGCAC	CTGTGCG	CCATCAG	CCCTG	GACCGT	ACTTGGT	CCATCACACAGGCCATCGAG 420	
Db	490	ATCGTGCAC	CTGTGTG	CCATCAG	CTTGG	ATCGT	TACTGGT	CCATCACCCAGGCCATAGAG 549	
QY	421	TACAACTGA	AGCGAC	CGCCGCG	CATCA	TGAGGCC	CATCAT	CATACCGTGTGGGTCAATC 480	
Db	550	TACAACTGA	AGCGAC	CGCCGCG	CATCA	TGAGGCC	CAATCAT	CGTCAACCGTGTGGGTCAATC 609	
QY	481	TCGGCCGTCA	TCTCTT	CCCCCG	CTCATCT	CCATCG	AGAAAG	GGCGCGCGCGCGGC 540	
Db	610	TCGGCCGTCA	TCTCTT	CCCCCG	CTCATCT	CCATCG	AGAAAG	GGCGCGCGCGCGGC 669	
QY	541	CCGAGCCGCG	CGCGCTG	CGAGATCA	ACGAC	CAAGAG	TGGTAC	GTCACTCGTCTG 600	
Db	670	CAGCAGCCG	CGCGCAAC	CGCGCTG	CGAGATCA	ACGAC	CAAGAG	TGGTACGTCACTCGTCT 729	
QY	601	TGCATCGG	CTCCTT	CTCGCT	CCCTGC	CTCAT	TGATC	CTGCTACGTGCGCATCTAC 660	
Db	730	TGCATCGG	CTCCTT	CTCGCT	CCCTGC	CTCAT	TGATC	CTGCTATGTGCGCATCTAT 789	
QY	661	CAGATCGC	CAAGCGT	CGACCG	CGTGC	CAAC	CGCGCG	GGGTCCGACGCGCGTCCGC 720	
Db	790	CAGATAGC	CAAGCGC	ACCGCG	CTGTC	CGCCCA	CGCGCG	GGGTCTCTGATCGCGCGCC 849	
QY	721	GGCGCGCG	GGGGCAC	CCGAGCG	CAGGCC	CAAC	CGTCTG	GGCCCCCGAGCGCGCGCGGC 780	
Db	850	GGCTGCGG	GGGGCG	CGCGAG	CGCAGG	CCCCA	ATGGC	CTAGGCCCCCGAGCGCGCGTGGGT 909	
QY	781	CCGGGGGCG	CAGAGG	CGCGA	ACCGCTG	CCCCA	CCCGAC	GTCAACGGCGCGCCCTGGCGAGCCC 840	

Db	910	CGCGTGGG	CGCGAG	CGCGCTA	CCCGTCC	AGTCA	ACGGTGC	CCCCGGG	GAGCCC 969
QY	841	GGCGCGCG	CGCGCGG	CACCG	CACCG	CGGTGG	ACCTGG	AGGAGAGCTCGTCTTCCGAC 900	
Db	970	GGCGCCGT	GGGCCCC	CGCGAC	CGTAC	GGGTGG	ACCTC	GAGGAGAGCTCCTCGTCTGAG 1029	
QY	901	CACGCCAG	CGCGCCT	CCAGG	CGCCCG	CAGAC	CCCGAG	CGCGGTCCCCGGGGCAAGGCAAG 960	
Db	1030	CACGCCAG	CGCGCCCC	CTGGG	CCCCCG	CAGGT	CCGAG	CGCGCCCTCGGGCCAAAGAGCAAG 1089	
QY	961	GCCCCGAG	CGAGCC	CAGGTGA	AGCCGG	CGCGAC	AGCCTG	CCCGCGCGCGCGCGCGCGGCGGCGACG 1020	
Db	1090	GCTCGGCG	GAGCCAG	GTAAG	CCCGGG	GACAG	CTGCC	ACGGCGCGCGCGCGCGCGCC 1149	
QY	1021	GGGATCGG	ACCGCG	CGCTGC	AGGGCG	GGGAG	GAGCG	CTCGGGGTGCCAAGGCGTCG 1080	
Db	1150	GGGCGGGG	CGCCCCG	CGACTG	GGGCC	CGGGAG	GCGCG	CGGGGTGCGCAAGGCGTCG 1209	
QY	1081	CGCTGGCG	GGGCGCAG	AAACCG	CGGAG	AAGCG	CTTAC	CGTTCGTCGTGGCCGTGGTCATC 1140	
Db	1210	CGCTGGCG	GGGAAG	CAGAA	CCCGG	AAGCG	CTTCA	CTTTCGTGCTGGCGGTGGTCATA 1269	
QY	1141	GGAGTGTTC	GTGGTGT	GCTGGT	TCCCTT	CTTCA	CCCTAC	ACGCTCACGGCCGCTCGGG 1200	
Db	1270	GGCGTGTTC	GTGGTGT	GCTGGT	TCCCTT	CTTCA	CCCTAC	ACGCTCACGGCCGCTAGGC 1329	
QY	1201	TGCTCCGT	GCCACG	CACGCT	CTTCAA	ATTCTT	CTTCTG	GTTCGGCTACTGCAACAGCTCG 1260	
Db	1330	TGCTCCGT	GCCGCC	CACTCT	CTTCAA	AGTTCTT	CTTCTG	GTTCGGCTACTGCAACAGCTCG 1389	
QY	1261	TTGAACCG	CGTCA	TACAC	CACTTT	CAAC	CACAG	ATTTCGCGCGCCCTTCAAGAAGATC 1320	
Db	1390	CTGAATCC	GGTTAT	CTAC	ACCAT	CTTCA	ATCAC	GACTTCCGCGCGCCCTTCAAGAAGATC 1449	
QY	1321	CTCTGT	CGGGG	GACAG	GGAAG	CGGAT	CGTG 1350		
Db	1450	CTCTGCCG	TGGG	A	CAGAA	ACGAT	CTGTG 1479		

RESULT 12	CPU25722	2291 bp	DNA	linear	ROD 05-SEP-2001
LOCUS	Cavia porcellus alpha-2A adrenoceptor gene, complete cds.				
DEFINITION	Cavia porcellus alpha-2A adrenoceptor gene, complete cds.				
ACCESSION	U25722				
VERSION	U25722.1	GI:818874			
KEYWORDS					
SOURCE	Cavia porcellus.				
ORGANISM	Cavia porcellus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.				
REFERENCE	1 (bases 1 to 2291)				
AUTHORS	Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and Regan,J.W.				
TITLE	Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and functional coupling to a CAMP-responsive reporter gene				
JOURNAL	Biochem. Pharmacol. 51 (3), 291-300 (1996)				
MEDLINE	96152573				
PUBMED	8573196				
REFERENCE	2 (bases 1 to 2291)				
AUTHORS	Richman,J.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona, Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson, AZ 85721, USA				
FEATURES	Location/Qualifiers				
source	1. .2291				
	/organism="Cavia porcellus"				
	/strain="Sasco Hartley albino"				
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	/clone=" (GP) alpha-2A"				
	49. .1401				
	CDS				

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PGEPAAGPRDAEALDLESSSSEHAERP PGARRPERGLRAKSKARASQVKPGDSLPR
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BASE COUNT 456 a 593 c 716 g 526 t

Query Match 84.0%; Score 1133.8; DB 10; Length 2291;
Best Local Similarity 90.9%; Pred. No. 1.8e-132;
Matches 1230; Conservative 0; Mismatches 117; Indels 6; Gaps 2;

QY	1	ATGGGCTCCCTGCAGCCGGACGGGGGCAACGCGAGCTGGAACGGGACCGAGGCGCCGGGG	60
Db	49	ATGGGCTCCCTCCAGCCAGACTCCGGCAACGCGAGCTGGAATGGGACCGAGGGCCCGGGA	108
QY	61	GGCGGCGCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGGC	120
Db	109	GGCGGCACCCGGGCGACCCCTTACTCCCTGCAGGTGACGGTGACGCTGGTGTGCCTGGTC	168
QY	121	GGCCTGCTCATGCTGCTCACCGTGTTCGGCAACGCTGCTCGTCATCATCGCCGTGTTACG	180
Db	169	GGCCTGCTCATACTGCTCACCGTGTTCGGCAACGTA CTGGTTCATCATCGCGGTGTTACC	228
QY	181	AGCGCGCGCTCAAGGCGGCCCCCAAACCTCTTCCTGGTGTCTCTGGCCTCGGCCGACATC	240
Db	229	AGCGCGCGCTCAAGGCGGCCCCAGAACCTCTTCCTGGTGTCTCTGGCCTCGGCAGACATT	288
QY	241	CTGGTGGCCACGCTCGTCATCCCTTTCTCGCTGGCCAAACGAGTCA TGGGCTACTGGTAC	300
Db	289	CTGGTGGCCACGCTCGTCATCCCTTCTCCTTGGCCAAACGAGTCA TGGGCTACTGGTAC	348
QY	301	TTCGGCAAGGCTTGGTCGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCGTCC	360
Db	349	TTTGGTAAGCGTGGTGCAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCGTCC	408
QY	361	ATCGTGCACTGTGCGCCATCAGCTGGACCGCTACTGTTCCATCATCACACAGGCCATCGAG	420
Db	409	ATCGTGCACTGTGCGCTATCAGCCTGGACCGCTACTGTTCCATCATCACGAGGCCATTGAG	468
QY	421	TACAACCTGAAGCGCACGCGCGCATCAAGGCCATCATCATCACCGTGTGGGTCA TC	480
Db	469	TACAACCTGAAGCGCACTCCGCGCGCATCAAGGCCATCATCGTCACCGTGTGGGTCA TC	528
QY	481	TCGGCGCTCATCTCCTTCCCGCGGTCATCTCCATCGAGAAAGGGCGGCGGCGCGGC	540
Db	529	TCGGCGCTCATCTCCTTCCCGCGGTCATCTCCTTTG---AGAAGGCGGCGGCGCGGG	585
QY	541	CCGAGCGCGCGGAGCGCGGTGCGAGATCAACGACCAAGAGTGGTACGTCA TCTCGTCG	600
Db	586	CAGCAGCTGCGGAGCCGCGCTCGAGATCAACGACCAAGAGTGGTACGTCA TCTCCTCC	645
QY	601	TGCATCGGCTCCTTCTTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGCGCATCTAC	660
Db	646	AGCATCGGCTCCTTCTTCGCGCCCTGCCTCATCATGATCCTGGTGTACGTGCGCATTTAC	705
QY	661	CAGATCGCAAGCGTGCACCCCGCTGCCACCCAGCCGCGGGGTCCGGACGC---CGTC	717
Db	706	CAAATAGCCAAGCGCCGACCCCGCTGCCACCCAGCCGCGGAGGTCCGGACGCCACGCC	765
QY	718	GCCGCGCGCGGGGGCACCCGAGCGCAGGCCCAACCGTCTGGGGCCCCGAGCGAGCGCG	777
Db	766	GCCGCGCGCGGGGGCGCCGAGCGCCGCCCAATGGCTGGGCTGGAGCGCGCGGTA	825
QY	778	GGCCCGGGGGCGCAGAGGCGCAACCGCTGCCCAACCGCTCAACGGCGCCCTGGCGGAG	837

Db	826	GGCCCCGGGGGGCGCGAGCCGAAACCTCTGCCACTCAGGTCAATGGCCGCCCGGGGAG	885
QY	838	CCCGCGCCCGCGCGCGCACACCGACCGCGCTGGACCTGGAGGAGAGCTCGTCTTCC	897
Db	886	CCCGCGCCCGCGCGCGCACGACGAGGCGCTGGACCTGGAGGAGAGCTCGTCTGTCG	945
QY	898	GACCACGCCGAGCGGCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCGGGGCAAGGC	957
Db	946	GAGCACGAGAGCGGCCCCCGGGGGCCCGAGACCCGAGCGCGGCTCCCGGGCCAAGAGC	1005
QY	958	AAGGCCGAGCGAGCCAGGTGAAGCCGGGCGACAGCCTGCCGCGCGCGGCGCGGGGCG	1017
Db	1006	AAGCGCGCGGAGCCAGGTGAAGCCCGCGACAGTCTGCCCCCGCGCGCGCGGGGCG	1065
QY	1018	ACGGGATCGGAGCCCGCTGCAGGGCCGGGAGGAGCGCGTCGSGGCTGCCAAGGC	1077
Db	1066	GCGGGTCCGGACTTCGGGTCCGGGCCGGGGGAGGAGCGTGGCGGGGGCGCTAAGGC	1125
QY	1078	TCGCGCTGGCGGGCGCAGAACCCGCGAGAACGCTTACGTTCTGCTGGCCGTGGTC	1137
Db	1126	TCGCGTTGGCGGGCGCAGAACCGTGAGAAAGCGCTTCACTTCTGCTGGCCGTGGTC	1185
QY	1138	ATCGGAGTGTCTGCTGGTGTCTGGTCCCTTCTTCAACCTTCTTCACTACAGCTCACGGCCGTC	1197
Db	1186	ATCGGAGTGTCTGCTGGTGTCTGGTCCCTTCTTCACTACAGCTCACGGCCGTG	1245
QY	1198	GGGTGCTCCGTGCCACGACGCTCTTCAAAATTCTTCTTCTGGTTCGGCTACTGCAACAGC	1257
Db	1246	GGCTGCTCGGTGCCGCGCACGCTCTTCAAGTCTTCTTCTGGTTGGCTACTGCAACAGC	1305
QY	1258	TCGTTGAACCCGTCATCTACACCATCTTCAACCACGATTTCGCGCGGCTTCAAGAAG	1317
Db	1306	TCCCTGAACCCGTCATCTACACCATCTTCAACCACGACTTCGCGCGGCTTCAAGAAG	1365
QY	1318	ATCCTCTGTGCGGGGACAGGAAGCGGATCGTG	1350
Db	1366	ATCCTCTGCGGGGACAGAAAGCGGATCGTG	1398

RESULT 13	RRU79031	1552 bp	mRNA	linear	ROD 14-JUN-2000
LOCUS	Rattus norvegicus alpha2D adrenergic receptor mRNA, complete cds.				
DEFINITION	U79031				
ACCESSION	U79031.1	GI:3282234			
VERSION					
KEYWORDS					
SOURCE	Rattus norvegicus.				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				
REFERENCE	1 (bases 1 to 1552)				
AUTHORS	Chalberg,S.C., Duda,T., Rhine,J.A. and Sharma,R.K.				
TITLE	Molecular cloning, sequencing and expression of an alpha				
	2-adrenergic receptor complementary DNA from rat brain				
JOURNAL	Mol. Cell. Biochem. 97 (2), 161-172 (1990)				
MEDLINE	91125329				
PUBMED	2177834				
REFERENCE	2 (bases 1 to 1552)				
AUTHORS	Wypijewski,K., Duda,T. and Sharma,R.K.				
TITLE	Structural, genetic and pharmacological identity of the rat alpha				
	2-adrenergic receptor subtype cA2-47 and its molecular				
	characterization in rat adrenal, adrenocortical carcinoma and				
	bovine retina				
JOURNAL	Mol. Cell. Biochem. 144 (2), 181-190 (1995)				
MEDLINE	95349560				
PUBMED	7623790				
REFERENCE	3 (bases 1 to 1552)				
AUTHORS	Venkataraman,V., Duda,T.M. and Sharma,R.K.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.				
	Dr., Stratford, NJ 08084, USA				

FEATURES		Location/Qualifiers				
source		1..1552	/organism="Rattus norvegicus"			
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		KWCEIYLALDVLVFCITSSIVHLCAISLDRYWSITQAIENLKRTPRIKAIIVTVWVI				
		SAVISFPPLISIEKGAGGQQPAEPSCKINDOKWYVISSSIGSFAPCLIMILVYVR				
		IYQIAKRRTRVPPSRPGDACSPAPGGADRRNGLGPERGAGTAGAEAPLPTQLNGA				
		PGEPAPTRPRDGDALDLESSSESHAERPQPGKPERGPRAKGTKASQVKPQDLSLPR				
		RGPGAAGPGASGSGQGERAGGAKASRWGRGRONREKRFTFVLAVVIGVVFVVCWFPFFF				
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		"				
BASE COUNT		244 a	504 c	498 g	306 t	
ORIGIN						
Query Match		82.0%;	Score 1106.8;	DB 10;	Length 1552;	
Best Local Similarity		88.7%;	Pred. No. 4.4e-129;			
Matches 1198;		Conservative 0;	Mismatches 152;	Indels 0;	Gaps 0;	
QY	1	ATGGGCTCCCTGCAGCCGGACGCGGGCAACGGAGCTGGAACGGGACCGAGCGCGGGG	60			
Db	1	ATGGGCTCCCTGCAGCGGATGCCGGCAATAGCAGCTGGAACGGACCGAGCGCCCGGA	60			
QY	61	GGCGGCGCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCC	120			
Db	61	GGCGGCACCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCT	120			
QY	121	GGCCTGTCTATGTGTCTACCGTGTTCGGGAACGTGCTCGTCATCATCGCCGTGTTCAAG	180			
Db	121	GGCCTGTCTATGTGTCTACCGTGTTCGGGAACGTGCTGGTTATTATCGAGTGTTCACC	180			
QY	181	AGCCGCGCGCTCAAGGCGCCCCAAAACCTCTTCCTGGTGTCTCTGGCTCGGCCGACATC	240			
Db	181	AGCCGCGCGCTCAAAAGCGCCCCAGAACCTCTTCCTGGTGTCTCTGGCTCAGCGGACATC	240			
QY	241	CTGGTGGCCACGCTCGTCATCCCTTTCTCGCTGGSCAACGAGGTCA TGGGCTACTGGTAC	300			
Db	241	CTGGTGGCCACGCTGGTCAATCCCTTTCTTTGSCAACGAGGTTATGGGCTACTGGTAC	300			
QY	301	TTCGGCAAGGCTTGGTGGGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCGTCC	360			
Db	301	TTTGGTAAGGTGGTGGGAGATCTACTTGGCCCTCGACGTGCTCTTTTGCACGTCGTCC	360			
QY	361	ATCGTGACCTGTGGCGCATCAGCCCTGGACCGGCTACTGGTCCATCACACAGGCCATCGAG	420			
Db	361	ATAGTGACCTGTGCGCCATCAGCCTTGACCGCTACTGGTCCATCACGAGGCCATCGAG	420			
QY	421	TACAACCTGAAGCGCACGCCGCGCGCATCAAGGCCATCATCATCCGTGTGGGTCAATC	480			
Db	421	TACAACCTGAAGCGCACGCCGCGCGCATCAAGGCCATCATTTGTCACCTGTGGGTCAATC	480			
QY	481	TCGGCGGTCAATCTCCTTCCCGCGCTCATCTCCATCAGAAAGAGGGCGGCGCGCGGC	540			
Db	481	TCGGCGGTCAATCTCCTTCCCGCGCACTCATCTCCATAGAAAGAGGGCGGTGGCGCGGG	540			
QY	541	CCGACGCCGCGGAGCCGCGTGGGAGATCAACGACAGAAAGTGGTACGTCACTCTCGTCG	600			
Db	541	CAGCAGCCGCGGAGCCGAGCTGCAAGATTAAACGACCAAGATGGTATGTCTATCTCGTCG	600			
QY	601	TGCATCGGCTCCTTCTTCGCTCCCTCATCATGATCCTGGTCTACGTGCGCATCTAC	660			
Db	601	TCCATCGGCTCCTTCTTCGCGCCTTGCCTCATCATGATCCTGGTCTACGTGCGTATCTAC	660			
QY	661	CAGATCGCCAAAGCGTCGCACCCCGGTGCCACCCCGGGGTCCCGACGCGGTGCGCC	720			
Db	661	CAGATCGCCAAAGCGTCGCACCCCGGTGCCACCCCGGGGTCCCGACGCGCTGTTCC	720			

QY	721	GCGCCGCGCGGGGGCACCGAGCGAGGCCCCAACGGTCTTGGGCCCCGAGCGCAGCGCGGC	780
Db	721	GCGCCGCGCGGGGGCGCCGATCGAGGCCCCAACGGGCTGGGCCCCGAGCGCGCGTGGT	780
QY	781	CCGGGGGCGCAGAGCCGAAACCGCTGCCACCCAGTCAACCGGCGCCCTTGGCGAGCCC	840
Db	781	ACCGGGGCGCGAGCCGAGCCGCTGCCACCCAGCTTAACGGGCCCCCGGGGAGCCC	840
QY	841	GCGCCGCGCGGCCCGCGCACACCGACGCGCTGGACCTGGAGGAGAGCTCGTCTTCGAC	900
Db	841	GCGCCACCCCGCCGCGACCGGGATGCGCTGGACCTAGAGGAGAGTTCTGTCGTCGAG	900
QY	901	CACGCCGAGCGGCTCCAGGGCCCCCGACACCCGAGCGCGGTCCCGGGGCAAGGCAAG	960
Db	901	CACGCCGAGCGGCCCCAGGGCCCCCGCAACCCGAGCGCGGTCCCCGGGCCAAGGGCAAG	960
QY	961	GCCGAGCGAGCCAGGTGAAGCCGGGCGACAGCTGCCGGCGCGCGGGCGCGGGCGGACG	1020
Db	961	ACCAAGCGAGCCAGGTGAAACCGGGGACAGTCTGCCGCGCGCGCGGCCCGGGGCTCG	1020
QY	1021	GGGATCGGACGCGGCTGCAGGGCCGGGGGAGGAGCGCTCGGGGCTGCCAAGGCGTCG	1080
Db	1021	GGCGCGGGGCTTCGGGGTCCGGGACAGGAGAGCGTGC CGGGGCGCCCAAAGCGTCG	1080
QY	1081	CGCTGGCGCGGCGCAGAACCCGCGAGAACGCTTCACGTTCTGCTGGCGCGTGGTCAATC	1140
Db	1081	CGCTGGCGCGGAGGAGAACCCGCGAGAACGCTTCACGTTCTGCTGGCGGTGGTGAATC	1140
QY	1141	GGAGTGTTCGTGTGTCTGGTTCCTTCTTTCACCTACACGCTCACGGCGCGTCGGG	1200
Db	1141	GGCGTGTTCGTGTGTGTGGTTCCTTCTTTCACCTACACGCTCATAGCGGTGCGG	1200
QY	1201	TGCTCCGTGCCACGACGCTCTTCAAATTTCTTCTTCTGTTTCGGTCTACTGCAACAGCTCG	1260
Db	1201	TGCCCCGTGCCCTACACGCTCTTCAAATTTCTTCTTCTGTTTCGGTCTACTGCAACAGCTCG	1260
QY	1261	TTGAACCCGGTCACTACACCATCTTCAACCAAGATTTCGCGCGCGCTTCAAGAAGATC	1320
Db	1261	CTGAACCTTGTATCTACACCATTTTCAACCAAGACTTCGCGCGCGCTTCAAGAAGATC	1320
QY	1321	CTCTGTGGGGGACAGGAAGCGGATCGTG	1350
Db	1321	CTCTGCCGTGGGACAGAAAGCGCATCGTG	1350

RESULT 14

RATRG20	RATRG20	1380 bp	DNA	linear	ROD 27-APR-1993
LOCUS	Rat alpha-2-adrenergic receptor protein (RG20) gene, complete cds.				
DEFINITION	Rat alpha-2-adrenergic receptor protein (RG20) gene, complete cds.				
ACCESSION	M62372				
VERSION	M62372.1 GI:206615				
KEYWORDS	alpha-2-adrenergic receptor; transmembrane protein.				
SOURCE	Rattus norvegicus (strain Sprague-Dawley) adult liver DNA.				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 1380)				
AUTHORS	Lanier,S.M., Downing,S., Duzic,E. and Homcy,C.J.				
TITLE	Isolation of rat genomic clones encoding subtypes of the alpha 2-adrenergic receptor. Identification of a unique receptor subtype				
JOURNAL	J. Biol. Chem. 266 (16), 10470-10478 (1991)				
MEDLINE	91244823				
PUBMED	1645350				
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Db	181	AGCCGCGGCTCAAAGCGCGCCCAAGACCTTCTCCTGGTGTCTCTGGCCTCAGCGGACATC	240		
QY	241	CTGGTGGCCACGCTCGTCATCCCTTTCTCGCTGGCCAACGAGGTCACTGGGCTACTGGTAC	300		
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QY	301	TTCCGCAAGGCTTGGTCCGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCTGCC	360		
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Db	721	GCGCCCGCGGGGCGCCGATCGCAGGCCAAACGGGTGGGCCCGAGCGCGCGTGGT	780
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Db	781	ACCGGGGCGCGAGGCCGAGCCGCTGCCACCCAGCTTAACGGCGCCCGGGGAGCCC	840
QY	841	GCGCCGCGCGGCGCGCACACCGACCGCTGGACCTGGAGGAGAGCTCGTCTTCCGAC	900
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QY	901	CACGCCGAGCGGCTCCAGGGCCCCGACACCCGAGCGCGGTCCCCGGGGCAAAGGCAAG	960
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QY	961	GCCCGAGCGCAGGTGAAGCCGGGCGACAGCCTGCCCGCGCGGGCCCCGGGGCAGC	1020
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Db	1021	GGCGCGGGGCTTCGGGTCGGGCGAGGAGGAGCGTGCCGGGGCGCCAAAGCGTCG	1080
QY	1081	CGTGGCGGGCGGAGAACCCGAGAACGCTTCACGTTCTGCTGGCGCTGCTCATC	1140
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QY	1141	GGAGTGTTCGTGGTGTCTGGTTCCCTTCTTTCACCTACACGCTCACGGCCGTCGGG	1200
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DEFINITION Bos taurus alpha2D adrenergic receptor gene, complete cds.
ACCESSION U79030
VERSION U79030.1 GI:3282232
KEYWORDS .
SOURCE Bos taurus.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 2923)
AUTHORS Venkataraman,V., Duda,T. and Sharma,R.K.
TITLE The bovine alpha 2D-adrenergic receptor gene: structure, expression
in retina, and pharmacological characterization of the encoded
receptor
JOURNAL Mol. Cell. Biochem. 177 (1-2), 113-123 (1997)
MEDLINE 9811113
PUBMED 9450652
REFERENCE 2 (bases 1 to 2923)
AUTHORS Venkataraman,V., Duda,T.M. and Sharma,R.K.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr Dr,
Stratford, NJ 08084, USA
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Job time : 20288.5 secs

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misc_feature	/note="assembly_fragment"	AUTHORS	Venkataraman,V., Duda,T.M. and Sharma,R.K.
misc_feature	9301..10747	TITLE	Direct Submission
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DEFINITION	Bos taurus alpha2D adrenergic receptor gene, complete cds.		
ACCESSION	U79030		
VERSION	U79030.1	GI:3282232	
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	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;		
	Bovidae; Bovinae; Bos.		
REFERENCE	1 (bases 1 to 2923)		
AUTHORS	Venkataraman,V., Duda,T. and Sharma,R.K.		
TITLE	The bovine alpha 2D-adrenergic receptor gene: structure, expression in retina, and pharmacological characterization of the encoded receptor		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 204317)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-358H2
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

2 (bases 1 to 204317)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
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Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (01-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 204317)

TITLE
JOURNAL
REFERENCE
AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
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Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
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O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
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Theodore,J., Topham,K., Travers,M., Travis,N., Triglio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 6, 2002 this sequence version replaced gi:21313866.

TITLE
JOURNAL
COMMENT

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L23807
Center clone name: 358 H 2

----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731
Consensus quality: 197709 bases at least Q40
Consensus quality: 200412 bases at least Q30
Consensus quality: 201149 bases at least Q20
Insert size: 210000; agarose-fp
Insert size: 202017; sum-of-contigs
Quality coverage: 6.3 in Q20 bases; agarose-fp
Quality coverage: 6.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 7387: contig of 7387 bp in length
* 7388 7487: gap of 100 bp
* 7488 7956: contig of 469 bp in length
* 7957 8056: gap of 100 bp
* 8057 9200: contig of 1144 bp in length
* 9201 9300: gap of 100 bp
* 9301 10747: contig of 1447 bp in length
* 10748 10847: gap of 100 bp
* 10848 12877: contig of 2030 bp in length
* 12878 12977: gap of 100 bp
* 12978 15172: contig of 2195 bp in length
* 15173 15272: gap of 100 bp
* 15273 18061: contig of 2789 bp in length
* 18062 18161: gap of 100 bp
* 18162 21071: contig of 2910 bp in length
* 21072 21171: gap of 100 bp
* 21172 24003: contig of 2832 bp in length
* 24004 24103: gap of 100 bp
* 24104 27175: contig of 3072 bp in length
* 27176 27275: gap of 100 bp
* 27276 30561: contig of 3286 bp in length
* 30562 30661: gap of 100 bp
* 30662 66767: contig of 36106 bp in length
* 66768 66867: gap of 100 bp
* 66868 73300: contig of 6433 bp in length
* 73301 73400: gap of 100 bp
* 73401 78880: contig of 5480 bp in length
* 78881 78980: gap of 100 bp
* 78981 89075: contig of 10095 bp in length
* 89076 89175: gap of 100 bp
* 89176 98581: contig of 9406 bp in length
* 98582 98681: gap of 100 bp
* 98682 105311: contig of 6630 bp in length
* 105312 105411: gap of 100 bp
* 105412 122788: contig of 17377 bp in length
* 122789 122888: gap of 100 bp
* 122889 132289: contig of 9401 bp in length
* 132290 132389: gap of 100 bp
* 132390 144818: contig of 12429 bp in length
* 144819 144918: gap of 100 bp
* 144919 159101: contig of 14183 bp in length
* 159102 159201: gap of 100 bp
* 159202 177288: contig of 18087 bp in length
* 177289 177388: gap of 100 bp
* 177389 201231: contig of 23843 bp in length
* 201232 201331: gap of 100 bp
* 201332 204317: contig of 2986 bp in length.

FEATURES
Location/Qualifiers
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1. .204317
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-358H2"
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1. .7387
/note="assembly_fragment"

Best Local Similarity 100.0%; Pred. No. 0.004; Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41
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Db 196299 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 196339

RESULT 9
AX350513
LOCUS AX350513 1350 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 25 from Patent WO0179561.
ACCESSION AX350513
VERSION AX350513.1 GI:18616108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 25 25-OCT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M. (US)
FEATURES Location/Qualifiers
source 1..1350
/organism="Homo sapiens"
/db_xref="taxon:9606" 220 t

BASE COUNT 199 a 489 c 442 g 220 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 6; Length 1350;
Best Local Similarity 97.6%; Pred. No. 0.035;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41
|||||
Db 730 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 770

RESULT 10
AF316894
LOCUS AF316894 1353 bp DNA linear PRI 07-FEB-2001
DEFINITION Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
ACCESSION AF316894
VERSION AF316894.1 GI:12698667
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling
JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE 20556293
PUBMED 10948191

REFERENCE 2 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606" 220 t
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IYQIAKRTRVPPSRGPDAAVAPPGGTERRPKGLGPERSAGPGGAEEPLPTQLNGA
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753
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Accession Number AF281308; polymorphic sequence encodes
Lys at amino acid 251"
/frequency="Caucasians 0.004; African-Americans 0.05"
/replace="C"

BASE COUNT 200 a 489 c 443 g 221 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 9; Length 1353;
Best Local Similarity 97.6%; Pred. No. 0.035;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41
|||||
Db 730 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 770

RESULT 11
MUSALP2ADB
LOCUS MUSALP2ADB 1454 bp DNA linear ROD 27-APR-1993
DEFINITION Mouse alpha-2 adrenergic receptor, complete cds.
ACCESSION M99377
VERSION M99377.1 GI:191882
KEYWORDS alpha-2 adrenergic receptor.
SOURCE Mus musculus (strain 129/Sv) DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 1454)
AUTHORS Link,R., Daunt,D., Barsh,G., Chruscinski,A. and Kobilka,B.
TITLE Cloning of two mouse genes encoding alpha 2-adrenergic receptor subtypes and identification of a single amino acid in the mouse alpha 2-C10 homolog responsible for an interspecies variation in antagonist binding
JOURNAL Mol. Pharmacol. 42 (1), 16-27 (1992)
MEDLINE 92342131
PUBMED 1353249

FEATURES Location/Qualifiers
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/strain="129/Sv"
/db_xref="taxon:10090"
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/db_xref="GI:191883"

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SAVISFPPLISIEKKGAGGQPPAEPSCKINDQWYVISSSIGSFAPCLIMILVYVR
IYQIAKRTRVPPSRGPDACSAPPGGARRPNGLPERGAGTGAEEPLPTQLNGA
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CDS       /product="alpha-2A adrenergic receptor"
          2085. .3437
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          /db_xref="GI:14029163"
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          KAWCEIYLALDVLFTSSIVHLCAISLDRYWSITQAI EYNLKRTPRRIKAIITVWVI
          SAVISFPPLISIEKKGGGGQPAPRCEINDOKWYVISSCIGSFAPCLIMILVYVR
          IYQIAKRRTVRPPSRGPDAAVAPGGTERRP NGLGPERSGAGPGA EAEPLPTQLNGA
          PGEPAPAGPRD TDALDLEESSSDHAERPPGPRRPERGPRGKGKARASQVKPGDSLPR
          RGPATGIGTPAAGPGEERVGA AKASRWGRQNRKRTFVLAVVIGVFVVCWFPFFF
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          "
BASE COUNT      555 a 1278 c 1136 g 643 t
ORIGIN
Query Match      100.0%; Score 41; DB 9; Length 3612;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 41
    |||||||
Db 2814 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 2854

RESULT 7
AF284095 LOCUS      3653 bp mRNA linear PRI 27-MAR-2001
DEFINITION Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds.
ACCESSION AF284095
VERSION AF284095.1 GI:13447750
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3653)
AUTHORS Mao,Z.-M., Tang,K., Li,B.-M. and Jing,N.-H.
TITLE Cloning and expression of human alpha-2A adrenergic receptor in
SY5Y cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3653)
AUTHORS Mao,Z.-M., Tang,K., Li,B.-M. and Jing,N.-H.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-2000) Shanghai Institute of Physiology, Chinese
Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China
FEATURES
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            880..2232
            /codon_start=1
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            KAWCEIYLALDVLFTSSIVHLCAISLDRYWSITQAI EYNLKRTPRRIKAIITVWVI
            SAVISFPPLISIEKKGGGGQPAPRCEINDOKWYVISSCIGSFAPCLIMILVYVR
            IYQIAKRRTVRPPSRGPDAAVAPGGTERRP NGLGPERSGAGPGA EAEPLPTQLNGA
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TYTLTAVGCSVPRTLKFKFFWFVGYCNSSLNPVIYTI FNHDFRRAFKKILCRGDRKRIV
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ORIGIN
Query Match      100.0%; Score 41; DB 9; Length 3653;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 41
    |||||||
Db 1609 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 1649

RESULT 8
AL158163 LOCUS      204908 bp DNA linear PRI 13-DEC-2001
DEFINITION Human DNA sequence from clone RP11-348N5 on chromosome 10, complete
sequence.
ACCESSION AL158163
VERSION AL158163.11 GI:17384427
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 204908)
AUTHORS Johnson,C.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
COMMENT On Dec 5, 2001 this sequence version replaced gi:16944857.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
RP11-348N5 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-348N5 The true
left end of clone RP11-479A21 is at 179266 in this sequence. The
true right end of clone RP11-313D6 is at 44800 in this sequence.
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Query Match      100.0%; Score 41; DB 9; Length 204908;

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AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C., Beschi,M. and Agabiti Rosei,E.
TITLE A search for genetic variability in the human alpha-2 adrenergic receptor on chromosome 10
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C., Beschi,M. and Agabiti Rosei,E.
TITLE Direct Submission
JOURNAL Submitted (29-APR-2000) Medical and Surgical Sciences, University of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REFERENCE 3 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C., Beschi,M. and Agabiti Rosei,E.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Medical and Surgical Sciences, University of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REMARK Sequence update by submitter
COMMENT On Aug 22, 2000 this sequence version replaced gi:9837145.
FEATURES Location/Qualifiers
source 1..1941
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/db_xref="taxon:9606"
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variation 261
/note="compared to sequence described in Bono et al, Gene Geography 10:151-160, 1996"
/replace="g"
519..1871
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BASE COUNT 305 a 676 c 624 g 336 t
ORIGIN
Query Match 100.0%; Score 41; DB 9; Length 1941;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1248 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCGGAGCG 1288
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RESULT 5
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LOCUS Human alpha 2 adrenergic receptor gene, complete cds.
DEFINITION M23533
ACCESSION M23533.1 GI:178195
VERSION adrenergic receptor; alpha-2 andrenergic receptor.
KEYWORDS Human DNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3604)
AUTHORS Fraser,C.M., Arakawa,S., McCombie,W.R. and Venter,J.C.
TITLE Cloning, sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells.
Evidence for independent pathways of receptor coupling to adenylate cyclase attenuation and activation
JOURNAL J. Biol. Chem. 264 (20), 11754-11761 (1989)

MEDLINE 89308571
PUBMED 2568356
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by W.R.McCombie, 30-MAR-1989.
FEATURES Location/Qualifiers
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1723..1728
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2078..3430
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BASE COUNT 555 a 1272 c 1134 g 643 t
ORIGIN
Query Match 100.0%; Score 41; DB 9; Length 3604;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCGGAGCG 41
|||||
Db 2807 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCGGAGCG 2847
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RESULT 6
AY032736
LOCUS Homo sapiens alpha-2A adrenergic receptor (ADR2AR) gene, complete cds.
DEFINITION AY032736.1 GI:14029162
ACCESSION AY032736
VERSION AY032736.1
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3612)
AUTHORS Liu,L. and Yuan,L.
TITLE Human alpha-2A adrenergic receptor gene and the genotype of -1296 nucleotide and motionsickness
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3612)
AUTHORS Liu,L. and Yuan,L.
TITLE Direct Submission
JOURNAL Submitted (17-APR-2001) Key Laboratory of Molecular Biology, General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036, China
FEATURES Location/Qualifiers
source 1..3612
/organism="Homo sapiens"
/db_xref="taxon:9606"
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FEATURES
source
Liggett, Stephen B. (US) ; Small, Kersten M. (US)
Location/Qualifiers
1. .1350
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/db_xref="taxon:9606"
BASE COUNT 199 a 490 c 441 g 220 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCAGCGAGCGAGCGCCCAACGGTCTGGGCCCCGAGCG 41
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Db 730 GGGGGCAGCGAGCGAGCGCCCAACGGTCTGGGCCCCGAGCG 770
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RESULT 2
AF281308
LOCUS
DEFINITION Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
ACCESSION AF281308
VERSION AF281308.1 GI:9652209
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)
JOURNAL
MEDLINE 20556293
PUBMED 10948191
REFERENCE 2 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA

FEATURES
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BASE COUNT 200 a 490 c 442 g 221 t
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Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCAGCGAGCGAGCGCCCAACGGTCTGGGCCCCGAGCG 41
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Db 730 GGGGGCAGCGAGCGAGCGCCCAACGGTCTGGGCCCCGAGCG 770
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RESULT 3
HUMADRA
LOCUS
DEFINITION Human platelet alpha-2-adrenergic receptor gene, complete cds.
ACCESSION M18415
VERSION M18415.1 GI:178191
KEYWORDS alpha-2-adrenergic receptor; alpha-adrenergic receptor.
SOURCE Human (lambda-EMBL 3 library) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1521)
AUTHORS Kobilka,B.K., Matsui,H., Kobilka,T.S., Yang-Feng,T.L., Francke,U., Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
TITLE Cloning, sequencing, and expression of the gene coding for the human platelet alpha 2-adrenergic receptor
Science 238 (4827), 650-656 (1987)
JOURNAL
MEDLINE 88042789
PUBMED 2823383
FEATURES
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BASE COUNT 223 a 546 c 499 g 253 t
ORIGIN Chromosome 10q23-q25.

Query Match 100.0%; Score 41; DB 9; Length 1521;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 788 GGGGGCAGCGAGCGAGCGCCCAACGGTCTGGGCCCCGAGCG 828
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RESULT 4
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LOCUS
DEFINITION Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
ACCESSION AF262016
VERSION AF262016.2 GI:9864781
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1941)

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: March 10, 2003, 18:28:11 ; Search time 607.543 Seconds
(without alignments)
1964.002 Million cell updates/sec

Title: US-09-636-259C-1_COPY_730_770
Perfect score: 41
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: gb_sy.*
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14: gb_vi.*
15: gb_vl.*
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18: em_in.*
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26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
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35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	41	100.0	1353	9	AF281308	AF281308 Homo sapi
3	41	100.0	1521	9	HUMADRA	M18415 Human plate
4	41	100.0	1941	9	AF262016	AF262016 Homo sapi
5	41	100.0	3604	9	HUMADRA2R	M23533 Human alpha
6	41	100.0	3612	9	AY032736	AY032736 Homo sapi
7	41	100.0	3653	9	AF284095	AF284095 Homo sapi
8	41	100.0	204908	9	AL158163	AL158163 Human DNA
9	39.4	96.1	1350	6	AX350513	AX350513 Sequence
10	39.4	96.1	1353	9	AF316894	AF316894 Homo sapi
11	34.6	84.4	1454	10	MUSALP2ADB	M99377 Mouse alpha
12	34.6	84.4	1552	10	RRU79031	U79031 Rattus norv
13	34.6	84.4	1728	4	PIGA2AR	J05652 Porcine alp
14	34.6	84.4	204317	2	AC113491	AC113491 Mus muscu
15	33	80.5	2923	4	BTU79030	U79030 Bos taurus
16	31.4	76.6	1380	10	RATRG20	M62372 Rat alpha-2
17	31.4	76.6	2291	10	CPU25722	U25722 Cavia porce
18	25	61.0	7353	6	AX344974	AX344974 Sequence
19	25	61.0	7353	6	AX348495	AX348495 Sequence
20	25	61.0	51146	2	AC090342	AC090342 Homo sapi
21	25	61.0	64711	2	AC114552	AC114552 Mus muscu
22	24.2	59.0	163156	2	AP004085	AP004085 Oryza sat
23	23.8	58.0	127128	2	AC105677	AC105677 Rattus no
24	23.6	57.6	11378	1	AE002058	AE002058 Deinococc
25	23.6	57.6	43147	1	SC4A10	AL109663 Streptomy
26	23.6	57.6	126141	2	AL356300	AL356300 Homo sapi
27	23.6	57.6	163801	2	AC025224	AC025224 Homo sapi
28	23.6	57.6	195076	9	AL391357	AL391357 Human DNA
29	23.4	57.1	1263	9	HSACAA1	X65140 H.sapiens A
30	23.4	57.1	26621	2	AC020878	AC020878 Mus muscu
31	23.4	57.1	39407	2	AC010648	AC010648 Homo sapi
32	23.4	57.1	65069	9	AC112706	AC112706 Homo sapi
33	23.4	57.1	100000	9	AP000498	AP000498 Homo sapi
34	23.4	57.1	144494	9	AC099534	AC099534 Homo sapi
35	23.4	57.1	176291	2	AC023583	AC023583 Homo sapi
36	23.4	57.1	182224	9	AC093116	AC093116 Homo sapi
37	23.4	57.1	188810	2	AC115398	AC115398 Rattus no
38	23.4	57.1	203230	2	AC026346	AC026346 Homo sapi
39	23.4	57.1	270000	9	AB026898	AB026898 Homo sapi
40	23.2	56.6	7353	6	AX344975	AX344975 Sequence
41	23.2	56.6	7353	6	AX348496	AX348496 Sequence
42	23.2	56.6	10543	1	AE007241	AE007241 Sinorhizo
43	23.2	56.6	315000	1	RME603644	AL603644 Rhizobium
44	23	56.1	1351	9	BC004261	BC004261 Homo sapi
45	23	56.1	1510	9	BC024233	BC024233 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS AX350512 Sequence 24 from Patent WO0179561. 1350 bp
DEFINITION AX350512
ACCESSION AX350512
VERSION AX350512.1 GI:18616107
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 24 25-OCT-2001;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: March 10, 2003, 18:24:01 ; Search time 48.9583 Seconds
(without alignments)
1885.930 Million cell updates/sec

Title: US-09-636-259C-1_COPY_730_770
Perfect score: 41
Sequence: 1 gggggcaccgagcgaggcc.....aacggtctgggccccgagcg 41

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues 4370478
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Match	Length	ID		
1	41	100.0	1350	23	AAI99917	Human alpha-2AAR e
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3	25	61.0	1733	24	ABQ47498	Oligonucleotide fo
C	25	61.0	1733	24	ABQ47499	Oligonucleotide fo
	25	61.0	7353	24	ABL32072	Human immune syste
C	25	61.0	7353	24	AAD28362	Human chemically t
	24	58.5	36	21	AAZ94312	Rat cholecystokini
C	24	58.5	37	21	AAZ94369	Human alpha 2A adr
	23.4	57.1	14855	22	ABA15164	Human nervous syst

10	23.4	57.1	22028	24	ABA933286	Human acetyl-Coenz
11	23.4	57.1	22028	24	ABA933288	Human acetyl-Coenz
C	12	23.2	1733	24	ABQ47500	Oligonucleotide fo
	13	23.2	1733	24	ABQ47501	Oligonucleotide fo
C	14	23.2	7353	24	ABL32073	Human immune syste
	15	23.2	7353	24	AAD28363	Human chemically t
16	22.6	55.1	978	23	ABL10491	Drosophila melanog
17	22	53.7	2176	23	ABL10759	Drosophila melanog
C	18	22	3036	22	AAF44733	Novel protein kina
	19	22	4705	23	ABL10758	Drosophila melanog
20	21.8	53.2	987	15	AAQ62089	L-fucose dehydroge
21	21.8	53.2	1056	24	ABL88015	DNA polymerase III
22	21.8	53.2	1056	24	ABL88016	DNA polymerase III
23	21.8	53.2	1457	24	ABK52770	cdNA encoding mito
24	21.8	53.2	1550	21	AAF21112	Human low adenosin
25	21.8	53.2	1550	21	AAA34990	Human adenosine re
26	21.8	53.2	3089	21	AAF21113	Human low adenosin
C	27	21.8	3089	21	AAA34991	Human adenosine re
	28	21.8	8254	22	ABA17475	Human nervous syst
29	21.6	52.7	135	20	AAZ23654	S. mobaraense tran
30	21.6	52.7	245	20	AAZ23652	Streptovorticilliu
31	21.6	52.7	1218	13	AAQ24197	Transglutaminase (
32	21.6	52.7	1322	13	AAQ24201	Transglutaminase (
33	21.6	52.7	1809	22	AAH20188	S. mobaraense IPO
34	21.6	52.7	1809	22	AAF86283	DNA encoding prepr
35	21.4	52.2	1436	20	AAK52471	Nucleotide sequenc
36	21.4	52.2	1732	22	AAK52471	Human polynucleoti
37	21.4	52.2	1763	22	AAK51487	Human polynucleoti
C	38	21.4	2787	19	AAV28914	Rat semaphorin Y e
	39	21.4	3195	19	AAV28913	Rat semaphorin Y e
C	40	21	344	21	AAK17573	Human secreted pro
C	41	21	51.2	22	AAK26210	Human cDNA encodin
C	42	21	1123	19	AAV20912	Human DBI/ACBP -li
	43	21	1239	14	AAQ50395	Lignin peroxidase
44	21	51.2	1239	14	AAQ61445	Lignin peroxidase
C	45	51.2	1337	22	AAI57930	Human polynucleoti

ALIGNMENTS

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ID	AAI99917
XX	AAI99917 standard; DNA; 1350 BP.
AC	AAI99917;
XX	
DT	18-FEB-2002 (first entry)
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DE	Human alpha-2AAR encoding DNA.
XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2AAR;
KW	GenBank Accession AF281308; chromosome 10; ds.
XX	
OS	Homo sapiens.
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FH	Key
FT	CDS
FT	1..1353
FT	/*tag= a
FT	/product= "alpha-2AAR"
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PN	WO200179561-A2.
XX	
PD	25-OCT-2001.
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PF	17-APR-2001; 2001WO-US12575.
XX	
PR	17-APR-2000; 2000US-0551744.
PR	10-AUG-2000; 2000US-0636259.
PR	19-OCT-2000; 2000US-0692077.

XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
XX WPI; 2001-611728/70.
DR P-PSDB; AAM52122.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Example 7; Page 151; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
CC or a site comprising (A) (ggggcgggcgcg) or (B) (ggggcgctgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (GenBank Accession AF281308).
XX
XX Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;
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Query Match 100.0%; Score 41; DB 23; Length 1350;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 41
Db 730 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 770
RESULT 2
AAI99918
ID AAI99918 standard; DNA; 1350 BP.
XX
AC AAI99918;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2AAR variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
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FT allele replace(753,C)

FT /*tag= b
XX WO200179561-A2.
PN
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
PI
XX WPI; 2001-611728/70.
DR P-PSDB; AAM52123.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Disclosure; Page 152; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
CC or a site comprising (A) (ggggcgggcgcg) or (B) (ggggcgctgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR variant
CC gene.
XX
SQ Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
Query Match 96.1%; Score 39.4; DB 23; Length 1350;
Best Local Similarity 97.6%; Pred. No. 0.00018;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 41
Db 730 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 770
RESULT 3
ABQ47498
ID ABQ47498 standard; DNA; 1733 BP.
XX
AC ABQ47498;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089.
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW

KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
OS Homo sapiens.
XX WO200218632-A2.
XX 07-MAR-2002.
XX 01-SEP-2001; 2001WO-EP10074.
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
PS This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX Sequence 1733 BP; 252 A; 211 C; 585 G; 685 T; 0 other;

Query Match 61.0%; Score 25; DB 24; Length 1733;
Best Local Similarity 75.6%; Pred. No. 13;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41
||||| ||||| ||| ||||| ||||| ||||| |||||
Db 990 GGGGGTATCGAGCGTAGGTTTAAACGGTTTGGGTTTCGAGCG 1030

RESULT 4
ABQ47499/c
ID ABQ47499 standard; DNA; 1733 BP.
XX ABQ47499;
AC
XX 12-JUL-2002 (first entry)
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34090.
DE Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.

XX Homo sapiens.
OS WO200218632-A2.
XX 07-MAR-2002.
XX 01-SEP-2001; 2001WO-EP10074.
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
PS This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX Sequence 1733 BP; 685 A; 585 C; 211 G; 252 T; 0 other;

Query Match 61.0%; Score 25; DB 24; Length 1733;
Best Local Similarity 75.6%; Pred. No. 13;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41
||||| ||||| ||| ||||| ||||| ||||| |||||
Db 744 GGGGGTATCGAGCGTAGGTTTAAACGGTTTGGGTTTCGAGCG 704

RESULT 5
ABL32072
ID ABL32072 standard; DNA; 7353 BP.
XX ABL32072;
AC
XX 26-MAR-2002 (first entry)
XX Human immune system associated gene SEQ ID NO: 45.
DE Human; immune system disease; cytosine methylation; antiasthmatic;
XX antiarteriosclerotic; antianaeamic; cytosatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
DR
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 45; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;

Query Match 61.0%; Score 25; DB 24; Length 7353;
Best Local Similarity 75.6%; Pred. No. 13;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCGCGAGCG 41
||||| |
Db 5730 GGGGGTATCGAGCGTAGGTTTAAACGGTTTGGGTTTCGAGCG 5770

RESULT 6
AAD28362
ID AAD28362 standard; DNA; 7353 BP.
XX
AC AAD28362;
XX
DT 22-APR-2002 (first entry)
XX
DE Human chemically treated genomic DNA #3.
XX
KW Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW drug abuse; migraine; ds.
XX
OS Homo sapiens.
XX
PN WO200202809-A2.
XX
PD 10-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07540.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2002-154759/20.
XX
PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -
XX
PS Claim 1; Page 32-36; 190pp; English.
XX
CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviour in schizophrenic
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
SQ Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;

Query Match 61.0%; Score 25; DB 24; Length 7353;
Best Local Similarity 75.6%; Pred. No. 13;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCGCGAGCG 41
||||| |
Db 5730 GGGGGTATCGAGCGTAGGTTTAAACGGTTTGGGTTTCGAGCG 5770

RESULT 7
AAZ94312/c
ID AAZ94312 standard; DNA; 36 BP.
XX
AC AAZ94312;
XX
DT 03-JUL-2000 (first entry)
XX
DE Rat cholecystokinin CCKB receptor PCR primer.
XX
KW G protein coupled receptor; cholecystokinin CCKB receptor;
KW rat; alpha-2A adrenergic receptor; human; screening; PCR primer;
KW ss.
XX
OS Rattus sp.
XX
PN WO200012704-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20011.
XX
PR 01-SEP-1998; 98US-0098704.
XX
PA (PAUS/) PAUSCH M H.
PA (LAIM/) LAI M.
PA (SILV/) SILVERMAN S.
PA (BIRS/) BIRSAN C.
PA (BAUM/) BAUMBAUCH W.
PA (TSEN/) TSENG E.
PA (KAJK/) KAJKOWSKI E M.
PA (OZEN/) OZENBERGER B A.
XX
PI Pausch MH, Lai M, Silverman S, Birsan C, Baumbauch W, Tseng E;
PI Kajkowski EM, Ozenberger BA;
XX

DR WPI; 2000-246753/21.

XX

PT Novel host cells comprising heterologous G protein-coupled receptor

PT modified to be constitutively active, useful for high throughput

PT screening assays for e.g. drugs, insecticides or nematocides -

XX

PS Example 3; Page 25; 75pp; English.

XX

CC This is the DNA sequence of a primer that was used in the PCR

CC amplification of DNA encoding the N-terminal portion (including 22

CC amino acids proximal to the 5th transmembrane domain) of rat

CC cholecystokinin CCKB receptor, a G protein coupled receptor (GPCR).

CC The PCR product was used in the construction of an intracellular

CC loop 3 (IC3) deleted CCKB receptor mutant. Deletion of a portion

CC of IC3 of mammalian GPCRs is correlated with improved functional

CC expression in yeast cells with retention of full ability to couple

CC to the heterotrimeric G protein. The invention relates to mutant

CC GPCRs with constitutively activating mutations that permit the

CC detection of the receptors' functional activity in the absence of

CC activating ligands, host cells that contain mutations that promote

CC the functional activity of the GPCRs, host cells expressing such

CC receptors, and vectors useful for making such cells. The host cells

CC are useful in high throughput screening assays for therapeutic drugs,

CC insecticides, nematocides etc., and are especially useful for assays

CC using orphan receptors.

XX

SQ Sequence 36 BP; 2 A; 15 C; 16 G; 3 T; 0 other;

Query Match 58.5%; Score 24; DB 21; Length 36;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCCCAACGGTCTGGGCCCCGAGCG 41

Db 36 GCCCAACGGTCTGGGCCCCGAGCG 13

RESULT 8

AAZ94369/c

ID AAZ94369 standard; DNA; 37 BP.

XX

AC AAZ94369;

XX

DT 03-JUL-2000 (first entry)

XX

DE Human alpha 2A adrenergic receptor PCR primer.

XX

KW G protein coupled receptor; GPCR; human;

KW alpha 2A adrenergic receptor; drug screening; PCR primer; ss.

XX

OS Homo sapiens.

XX

PN WO200012705-A2.

XX

PD 09-MAR-2000.

XX

PF 01-SEP-1999; 99WO-US20013.

XX

PR 01-SEP-1998; 98US-0098704.

XX

PA (PAUS/) PAUSCH M H.

PA (WESS/) WESS J.

XX

PI Pausch MH, Wess J;

XX

DR WPI; 2000-246754/21.

XX

PT New G protein-coupled receptors with a mutation in an intracellular

PT domain, useful for high throughput screening assays for e.g. drugs,

PT insecticides or nematocides -

XX

PS Example 5; Page 16; 37pp; English.

XX

CC This is the DNA sequence of a primer that was used in the PCR

CC amplification of DNA encoding the N-terminal portion (including 39

CC amino acids proximal to the 5th transmembrane domain) of human

CC alpha 2A adrenergic receptor, a G protein coupled receptor (GPCR).

CC The PCR product was used in the construction of an intracellular

CC loop 3 (IC3) deleted receptor mutant. Deletion of a portion

CC of IC3 of mammalian GPCRs is correlated with improved functional

CC expression in yeast cells with retention of full ability to couple

CC to the heterotrimeric G protein. The invention provides modified

CC GPCRs having a mutation in IC3 that results in an improved functional

CC response in cell-based assays. The modification promotes growth

CC stimulation by a GPCR agonist, especially by improving coupling

CC between the receptor and a heterotrimeric G protein. Polynucleotides

CC encoding the mutated GPCR, chimeric GPCR, vectors and host cells are

CC also claimed. The modified GPCRs can be used in improved high

CC throughput screening assays (especially in yeast cells) for

CC therapeutic drugs, insecticides, nematocides etc.

XX

SQ Sequence 37 BP; 2 A; 15 C; 17 G; 3 T; 0 other;

Query Match 58.5%; Score 24; DB 21; Length 37;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCCCAACGGTCTGGGCCCCGAGCG 41

Db 37 GCCCAACGGTCTGGGCCCCGAGCG 14

RESULT 9

ABA15164

ID ABA15164 standard; DNA; 14855 BP.

XX

AC ABA15164;

XX

DT 23-JAN-2002 (first entry)

XX

DE Human nervous system related polynucleotide SEQ ID NO 7495.

XX

KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;

KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

KW antiparkinsonian; antispasmodic; antianaemic; antiarthritic; cancer;

KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;

KW antiallergic; antidiabetic; antidiarrhoeal; anticonvulsant; antifungal;

KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;

KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX

OS Homo sapiens.

XX

PN WO200159063-A2.

XX

PD 16-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US01334.

XX

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.

PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-02559678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
DR
XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
PS Disclosure; SEQ ID NO 7495; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AB11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.

```
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 14855 BP; 3335 A; 3554 C; 4013 G; 3953 T; 0 other;

Query Match          57.1%; Score 23.4; DB 22; Length 14855;
Best Local Similarity 73.2%; Pred. No. 44;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 GGGGGCACCAGCGCAGGCCCAACGGTCTGGGCCCGGAGCG 41
    ||||| | ||||| | ||||| | ||||| | ||||| |
Db 265 GGCGGCTTCAAGGTGAGGCCCGGAGGCTCTGGGCCCGAGTG 305

RESULT 10
ABA93286
ID ABA93286 standard; DNA; 22028 BP.
XX
AC ABA93286;
XX
DT 22-APR-2002 (first entry)
XX
DE Human acetyl-Coenzyme A acyltransferase 1 gene SEQ ID NO:1.
XX
KW Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22;
KW peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype;
KW single nucleotide polymorphism; polymorphic variant; enzyme; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(3546,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(3637,A)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(4033,T)
FT /*tag= c
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(4157,T)
FT /*tag= d
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(4176,A)
FT /*tag= e
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(4276,C)
FT /*tag= f
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(9110,G)
FT /*tag= g
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(9182,A)
FT /*tag= h
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(9600,G)
FT /*tag= i
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(11702,T)
FT /*tag= j
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(11756,C)
FT /*tag= k
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(13390,T)
FT /*tag= l
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(1441,G)
FT /*tag= m
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(14872,C)
FT /*tag= n
```

```
FT variation /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(14931,C)
FT /*tag= o
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(15471,C)
FT /*tag= p
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(15486,G)
FT /*tag= q
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(18004,T)
FT /*tag= r
FT /standard_name= "single nucleotide polymorphism (SNP)"
FT replace(18192,T)
FT /*tag= s
FT /standard_name= "single nucleotide polymorphism (SNP)"
XX
PN WO200187903-A2.
XX
XX 22-NOV-2001.
PD
XX
PF 03-MAY-2001; 2001WO-US14330.
XX
PR 18-MAY-2000; 2000US-205022P.
XX
PA (GENA-) GENA1SSANCE PHARM INC.
PA (DUDA/) DUDA A E.
XX
PI Chew A, Koshy B;
XX
DR WPI; 2002-164134/21.
XX
XX Isolated polynucleotide, comprising a polymorphic variant of the
PT acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A
PT thiolase) gene useful for providing haplotype information and in
PT therapy for treating related disorders -
XX
PS Claim 19; Fig 1A-I; 93pp; English.
XX
CC The present invention describes a polypeptide (I) which is a polymorphic
CC variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal
CC 3-oxoacyl-Coenzyme A thiolase) ACAA1 protein (ABB05516). ACAA1 is located
CC on chromosome 3p23-p22. (I) can be encoded by ABA93286 (or ABA93288)
CC where the sequence comprises one of the haplotypes shown in Table 4 or
CC one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are
CC given in the specification. The polynucleotide encoding ACAA1 can be used
CC for providing haplotype and genotype information of an individual.
CC Furthermore, the polynucleotide is useful for the treatment of disorders
CC related to its abnormal expression or function. The present sequence
CC represents the human ACAA1 gene, featuring all the single nucleotide
CC polymorphisms (SNP) possible, from the present invention.
XX
SQ Sequence 22028 BP; 4811 A; 5599 C; 6137 G; 5481 T; 0 other;

Query Match          57.1%; Score 23.4; DB 24; Length 22028;
Best Local Similarity 73.2%; Pred. No. 44;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 GGGGGCACCAGCGCAGGCCCAACGGTCTGGGCCCGGAGCG 41
    ||||| | ||||| | ||||| | ||||| | ||||| |
Db 4199 GGCGGCTTCAAGGTGAGGCCCGGAGGCTCTGGGCCCGAGTG 4239

RESULT 11
ABA93288
ID ABA93288 standard; DNA; 22028 BP.
XX
AC ABA93288;
XX
DT 22-APR-2002 (first entry)
XX
DE Human acetyl-Coenzyme A acyltransferase 1 gene SEQ ID NO:99.
XX
```


PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPiG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;

Query Match 56.6%; Score 23.2; DB 24; Length 1733;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CACCGAGCGCAGGCCCAACGGTCTGGGCCCGAGCG 41
||||| |||| ||||| ||| ||||| ||
Db 995 CACCGAACGCAAAACCCCAACGATCTAAACCCCGAACG 1030

RESULT 14
ABL32073/c
ID ABL32073 standard; DNA; 7353 BP.
XX
XX ABL32073;
AC
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 46.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
XX
XX WO200200928-A2.
PN
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.

XX 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2002-130909/17.
XX
DR Nucleic acid comprising fragment of chemically modified gene, useful
XX for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
PT
XX Claim 1; SEQ ID NO 46; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match 56.6%; Score 23.2; DB 24; Length 7353;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CACCGAGCGCAGGCCCAACGGTCTGGGCCCGAGCG 41
||||| |||| ||||| ||| ||||| ||
Db 1619 CACCGAACGCAAAACCCCAACGATCTAAACCCCGAACG 1584

RESULT 15
AAD28363/c
ID AAD28363 standard; DNA; 7353 BP.
XX
XX AAD28363;
AC
XX
DT 22-APR-2002 (first entry)
XX
DE Human chemically treated genomic DNA #4.
XX
KW Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW drug abuse; migraine; ds.
XX
OS Homo sapiens.
XX
XX WO200202809-A2.
PN
XX
PD 10-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07540.
PF
XX
XX 30-JUN-2000; 2000DE-1032529.
PR
XX 01-SEP-2000; 2000DE-1043826.
XX
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2002-154759/20.
XX
PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -

XX Claim 1; Page 36-40; 190pp; English.
PS
XX
CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenic
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match 56.6%; Score 23.2; DB 24; Length 7353;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CACCGAGCGCAGGCCCAACGGTCTGTGGCCCCCGAGCG 41
||||| ||||| ||||| ||| ||||| ||
Db 1619 CACCGAACGCAACCCCAACGATCTAAACCCCGAACG 1584

Search completed: March 10, 2003, 18:59:36
Job time : 56.9583 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:31:11 ; Search time 2.88857 Seconds
(without alignments)
4352.932 Million cell updates/sec

Title: US-09-636-259C-1_COPY_730_770

Perfect score: 41

Sequence: 1 gggggcaccgagcgaggcc.....aacggtctggcccgagcg 41

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.6	52.7	225	1	US-08-136-993-6
2	21.6	52.7	1218	1	US-08-136-993-8
3	21.6	52.7	1322	1	US-08-136-993-12
4	21.4	52.2	1436	4	US-09-199-637A-131
5	21	51.2	1123	1	US-08-700-626-2
6	20.8	50.7	598	4	US-08-998-416-1090
7	20.8	50.7	686	4	US-08-998-416-1040
8	20.6	50.2	35060	3	US-08-814-095-7
9	20.4	49.8	232	6	5318899-25
10	20.4	49.8	294	6	5318899-27
11	20.4	49.8	9775	4	US-08-977-171-1
12	20.4	49.8	9934	4	US-08-977-171-2
13	20.2	49.3	2036	3	US-08-923-454A-17
14	19.8	48.3	51	1	US-07-690-983D-17
15	19.8	48.3	54	1	US-07-690-983D-27
16	19.8	48.3	4190	3	US-08-938-291A-2
17	19.8	48.3	44377	2	US-08-804-227C-7
18	19.8	48.3	44377	2	US-08-804-198-1
19	19.8	48.3	4403765	4	US-09-103-840A-2
20	19.8	48.3	4411529	4	US-09-103-840A-1
21	19.6	47.8	1008	4	US-09-091-097-38
22	19.4	47.3	1556	4	US-09-043-937A-3
23	19.4	47.3	33529	4	US-09-144-085-3
24	19.4	47.3	4403765	4	US-09-103-840A-2
25	19.2	46.8	856	1	US-08-117-373-10
26	19.2	46.8	4724	1	US-08-404-665-3
27	19.2	46.8	4724	1	US-08-404-671-3

28	19.2	46.8	4724	1	US-08-404-781-3	Sequence 3, Appli
29	19.2	46.8	6763	2	US-08-756-506-23	Sequence 23, Appl
30	19.2	46.8	8517	3	US-08-827-208-1	Sequence 1, Appli
31	19.2	46.8	8517	4	US-09-500-358-1	Sequence 1, Appli
32	19.2	46.8	8517	4	US-09-498-809-1	Sequence 1, Appli
33	19.2	46.8	10807	1	US-08-206-176-7	Sequence 7, Appli
34	19.2	46.8	10807	2	US-08-756-506-5	Sequence 5, Appli
35	19.2	46.8	50937	4	US-09-428-517-1	Sequence 1, Appli
36	19	46.3	459	2	US-08-387-942C-31	Sequence 31, Appl
37	19	46.3	3164	1	US-08-188-228-49	Sequence 49, Appl
38	19	46.3	3164	1	US-08-332-643-43	Sequence 43, Appl
39	19	46.3	3164	1	US-08-332-638-49	Sequence 49, Appl
40	19	46.3	6803	3	US-08-665-259-19	Sequence 19, Appl
41	19	46.3	6803	3	US-08-762-500-19	Sequence 19, Appl
42	19	46.3	12588	2	US-08-387-942C-1	Sequence 1, Appli
43	19	46.3	35100	2	US-08-770-379-19	Sequence 19, Appl
44	19	46.3	35100	4	US-08-757-669A-19	Sequence 19, Appl
45	19	46.3	35100	4	US-09-230-371A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-08-136-993-6

; Sequence 6, Application US/08136993

; Patent No. 5420025

; GENERAL INFORMATION:

; APPLICANT: Takagi, Hiroshi

; APPLICANT: Arafuka, Shino

; APPLICANT: Matsui, Hiroshi

; APPLICANT: Washizu, Kinya

; APPLICANT: Ando, Keiichi

; APPLICANT: Koikeda, Satoshi

; TITLE OF INVENTION: Recombinant transglutaminase

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas

; STREET: 2100 Pennsylvania Avenue

; CITY: N.W.

; STATE: Washington, D.C.

; COUNTRY: U.S.A.

; ZIP: 20037-3202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/136,993

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/777,447

; FILING DATE:

; APPLICATION NUMBER: JP 2-282566

; FILING DATE: 19-OCT-1990

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-293-7060

; TELEFAX: 202-293-7860

; TELEX: 6491103

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 225 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-136-993-6

Query Match 52.7%; Score 21.6; DB 1; Length 225;

Best Local Similarity 75.0%; Pred. No. 42;

Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCC 36
|| || || || || || || || || || || || || || || ||
pB 189 GGCCGGTTTCGAGCGCGGCSCCGTCGTTCGGGGCCCC 224

RESULT 2

US-08-136-993-8
; Sequence 8, Application US/08136993
; Patent No. 5420025
; GENERAL INFORMATION:
; APPLICANT: Takagi, Hiroshi
; APPLICANT: Arafuka, Shino
; APPLICANT: Matsui, Hiroshi
; APPLICANT: Washizu, Kinya
; APPLICANT: Ando, Keiichi
; APPLICANT: Koikeda, Satoshi
; TITLE OF INVENTION: Recombinant transglutaminase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue
; CITY: N.W.
; STATE: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,993
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/777,447
FILING DATE:
APPLICATION NUMBER: JP 2-282566
FILING DATE: 19-OCT-1990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-293-7060
TELEFAX: 202-293-7860

; INDEX: 0431103
: INFORMATION FOR SEQ ID NO: 8::; INFORMATION FOR SEQ ID NO:
: SEQUENCE CHARACTERISTICS:; SEQUENCE CHARACTERISTICS: 1218 base pairs
; LENGTH: 1218 base pairs

NAME: nucleic acid

STRANDEDNESS: double

: TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

115-08-136-993-8

Query Match	52.7%;	Score 21.6;	DB 1;	Length 1218;
Best Local Similarity	75.0%;	Pred. No. 41;		
Matches 27;	Conservative	0;	Mismatches 9;	Indels 0;
				Gaps 0;

Qy 1 GGGGCGACGAGCGCAGGCCAACGGTCTGTGGGCACC 36
 ||| | | | | |
pB 189 GGCCGCTTCGAGCGCCGGCCCCGTGCTTCGGGGCCCC 222
 ||| | | | | |

RESULT 3

US-08-136-993-12
; Sequence 12, Application US/08136993
; Patent No. 5420025
; GENERAL INFORMATION:
; APPLICANT: Takagi, Hiroshi
; APPLICANT: Arafuka, Shino
; APPLICANT: Matsui, Hiroshi
; APPLICANT: Washizu, Kinya
; APPLICANT: Ando, Keiichi
; APPLICANT: Koikeda, Satoshi

```

; TITLE OF INVENTION: Recombinant transglutaminase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue
; CITY: N.W.
; STATE: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,993
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/777,447
; FILING DATE:
; APPLICATION NUMBER: JP 2-282566
; FILING DATE: 19-OCT-1990
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-293-7060
; TELEFAX: 202-293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1322 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Streptovorticillum sp.
; IMMEDIATE SOURCE:
; CLONE: pTV118 NcoI
;
US-08-136-993-12

```

Query Match	52.7%;	Score 21.6;	DB 1;	Length 1322;
Best Local Similarity	75.0%;	Pred. No. 41;		
Matches 27; Conservative	0;	Mismatches	9;	Indels 0

QY 1 GGGGACCGAGCGCAGGCCCAACGGTCTGGGCCCC 36
 || | | | | | | | | | | | | |
pb 282 GGCGGTTCGAGCGCGGCCCGTCGTTCGGGGCCCC 317

RESULT 4

```

US-09-199-637A-131
; Sequence 131, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 1436

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STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1040:
SEQUENCE CHARACTERISTICS:
LENGTH: 686 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1635UP
US-08-998-416-1040

Query Match 50.7%; Score 20.8; DB 4; Length 686;
Best Local Similarity 70.0%; Pred. No. 75;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCAGGCCCAACGGTCTGGGCCCGGAGC 40
   || ||||| ||||| ||||| ||||| |||||
Db 233 GGCAGCACCAGCGCCTGGCCCAACAGGCTCGACGCGAGC 272

RESULT 8
US-08-814-095-7
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Cosmid including ACHE
; DESCRIPTION: promotor, ACHE gene and ARS gene"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 7q22
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 4089..22464
; OTHER INFORMATION: /function= "ACHE Promotor"
; OTHER INFORMATION: /standard_name= "ACHE Promotor"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 22465..22537
; OTHER INFORMATION: /function= "non-translated"
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: 24090..25177
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "(translation start:
; OTHER INFORMATION: 24110)"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: 25524..26009
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: 27005..27274
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 4
; FEATURE:
; NAME/KEY: exon
; LOCATION: 27255..28007
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 5
; FEATURE:
; NAME/KEY: terminator
; LOCATION: 27385..27387
; FEATURE:
; NAME/KEY: exon
; LOCATION: 28008..28129
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 6
; FEATURE:
; NAME/KEY: terminator
; LOCATION: 28129..28131
; FEATURE:
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;
; NAME/KEY: exon
; LOCATION: complement (34528..34895)
; OTHER INFORMATION: /function= "arsenite resistance"
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (34092..34358)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (33779..33963)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (33493..33591)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 4
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (33297..33408)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 5
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (32959..33094)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 6
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (32569..32628)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 7
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (32386..32468)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 8
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (31894..32080)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 9
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (31363..31534)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 10
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (31131..31284)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 11
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (30816..31011)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 12
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (30470..30626)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 13
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (30187..30274)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 14
; FEATURE:
; NAME/KEY: exon
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; LOCATION: complement (29945..30073)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 15
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (29664..29856)
; OTHER INFORMATION: /gene= "ARS"
; OTHER INFORMATION: /number= 16
; US-08-814-095-7
;
; Query Match 50.2%; Score 20.6; DB 3; Length 35060;
; Best Local Similarity 74.3%; Pred. No. 79;
; Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
;
; QY 2 GGGGCACCGAGCGCGCCCAACGGTCTGGGCCCC 36
; ||||| ||||| ||||| ||||| ||||| |||||
; Db 22583 GGGGCACCGTGGCTCCCGAGGGGTCCAGGCCCC 22617
;
; RESULT 9
; 5318899-25/c
; Patent No. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.;WOLF, DAVID L.;CHARO,
; ISRAEL F.
; TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/483,229
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 418,028
; FILING DATE: 06-OCT-1989
; APPLICATION NUMBER: 367,509
; FILING DATE: 16-JUN-1989
; SEQ ID NO:25:
; LENGTH: 232
; 5318899-25
;
; Query Match 49.8%; Score 20.4; DB 6; Length 232;
; Best Local Similarity 71.1%; Pred. No. 1e+02;
; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
;
; QY 4 GGCACCGAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 41
; ||||| ||||| ||||| ||||| ||||| |||||
; Db 124 GGCACGTGATCACAGCACAGACCGTCTGCGCACTGAGCG 87
;
; RESULT 10
; 5318899-27/c
; Patent No. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.;WOLF, DAVID L.;CHARO,
; ISRAEL F.
; TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/483,229
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 418,028
; FILING DATE: 06-OCT-1989
; APPLICATION NUMBER: 367,509
; FILING DATE: 16-JUN-1989
; SEQ ID NO:27:
; LENGTH: 294
; 5318899-27
;
; Query Match 49.8%; Score 20.4; DB 6; Length 294;
; Best Local Similarity 71.1%; Pred. No. 1e+02;
; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
;
; QY 4 GGCACCGAGCGCGAGCCCAACGGTCTGGGCCCCGAGCG 41
; ||||| ||||| ||||| ||||| ||||| |||||
; Db 186 GGCACGTGATCACAGCACAGACCGTCTGCGCACTGAGCG 149
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RESULT 11
US-08-977-171-1/c
; Sequence 1, Application US/08977171
; Patent No. 6232112
; GENERAL INFORMATION:
; APPLICANT: CATCHESIDE, DAVID E.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION
; TITLE OF INVENTION: OF DNA
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6232112west Center, 90 South 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,171
; FILING DATE: 24-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 10552.13US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9775 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-977-171-1
Query Match 49.8%; Score 20.4; DB 4; Length 9775;
Best Local Similarity 71.1%; Pred. No. 95;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGCAGGCCAACCGTCTGGGCCCCGAGC 40
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2547 GGGCACCAGCGCAGGCCAACCGTCTGGGCCCCAACC 2510

RESULT 12
US-08-977-171-2/c
; Sequence 2, Application US/08977171
; Patent No. 6232112
; GENERAL INFORMATION:
; APPLICANT: CATCHESIDE, DAVID E.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION
; TITLE OF INVENTION: OF DNA
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6232112west Center, 90 South 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,171
; FILING DATE: 24-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 10552.13US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9934 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-977-171-2
Query Match 49.8%; Score 20.4; DB 4; Length 9934;
Best Local Similarity 71.1%; Pred. No. 95;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGCAGGCCAACCGTCTGGGCCCCGAGC 40
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2651 GGGCACCAGCGCAGGCCAACCGTCTGGGCCCCAACC 2614

RESULT 13
US-08-923-454A-17/c
; Sequence 17, Application US/08923454A
; Patent No. 6004794
; GENERAL INFORMATION:
; APPLICANT: Creasy, Caretha
; APPLICANT: Livi, George
; APPLICANT: Karran, Eric
; APPLICANT: Clinkenbeard, Helen
; APPLICANT: Browne, Michael
; APPLICANT: Southan, Christopher
; TITLE OF INVENTION: HUMAN SERINE PROTEASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,454A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025436
; FILING DATE: 06-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50547
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2036 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORIGINAL SOURCE: Feature polymorphism at 1325
US-08-923-454A-17

Query Match 49.3%; Score 20.2; DB 3; Length 2036;
Best Local Similarity 68.3%; Pred. No. 1.1e+02;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCGGCCCAACGGTCTGGGCCCCCGAGCG 41
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 190 GCGGGCAGCGCGCGGCTCGCAGCGGTCTGGGCACCCGCG 150

RESULT 14
US-07-690-983D-17
; Sequence 17, Application US/07690983D
; Patent No. 5403586
; GENERAL INFORMATION:
; APPLICANT: RUSSELL-JONES, Gregory J.
; APPLICANT: STEWART, Andrew G.
; APPLICANT: TSONIS, Con G.
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/690,983D
; FILING DATE: 25-JUN-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU90/00373
; FILING DATE: 24-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/148 CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA
; IMMEDIATE SOURCE:
; CLONE: pBTA 735
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: 13..42
; OTHER INFORMATION: /note= "Coding sequence for LHRH"
; TELEX:
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..51
US-07-690-983D-17

Query Match 48.3%; Score 19.8; DB 1; Length 51;
Best Local Similarity 69.2%; Pred. No. 1.7e+02;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3 GGGCACCGAGCGCGGCCCAACGGTCTGGGCCCCGAGCG 41
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Db 3 GGCCCCGAGCACTGGTCATATGGTCTGCGTCCCGGGG 41

RESULT 15
US-07-690-983D-27
; Sequence 27, Application US/07690983D
; Patent No. 5403586
; GENERAL INFORMATION:
; APPLICANT: RUSSELL-JONES, Gregory J.
; APPLICANT: STEWART, Andrew G.
; APPLICANT: TSONIS, Con G.
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/690,983D
; FILING DATE: 25-JUN-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU90/00373
; FILING DATE: 24-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/148 CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA
; IMMEDIATE SOURCE:
; CLONE: pBTA 740
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..54
;
; NAME/KEY: misc feature
; LOCATION: 13..42
; OTHER INFORMATION: /note= "Coding sequence for LHRH"
; IMMEDIATE SOURCE:
; CLONE: pBTA 735
; FEATURE:
US-07-690-983D-27
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Query Match 48.3%; Score 19.8; DB 1; Length 54;
Best Local Similarity 69.2%; Pred. No. 1.7e+02;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 3 GGGCACCGAGCGCAGGCCCAACGGTCTGTGGGCCCCCGAGCG 41
||| ||||| ||| ||||| ||||| ||||| ||||| |||||
Db 6 GGCCCCCGAGCACTGGTTCATATGGTCTGCGTCCCGGGG 44

Search completed: March 11, 2003, 07:41:04
Job time : 20.8886 secs


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; APPLICANT: MOMOSE, HARUO
; TITLE OF INVENTION: A METHOD OF PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 220567USOCONT
; CURRENT APPLICATION NUMBER: US/10/124,429
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/JP00/07135
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: JP 11-295649
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1809
; TYPE: DNA
; ORGANISM: Streptovorticillum mobaraense
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (578)..(1798)
; OTHER INFORMATION:
US-10-124-429-3

Query Match      52.7%; Score 21.6; DB 9; Length 1809;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGTGGGCCCC 36
Db      769 GGCGGCTTCGAGCGCGCGCGCGTCTGTTCCGGGCCCC 804

RESULT 3
US-09-975-719-131
; Sequence 131, Application US/09975719
; Publication No. US20030022349A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Rahme, Laurence G.
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361003
; CURRENT APPLICATION NUMBER: US/09/975,719
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 09/199,637
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-975-719-131

Query Match      52.2%; Score 21.4; DB 9; Length 1436;
Best Local Similarity 80.6%; Pred. No. 52;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3 GGGCACCGAGCGCAGGCCCAACGGTCTGTGGGC 33
Db      1187 GGCGCGCAGCGCAGCAGCAACCGCTGGGC 1217

RESULT 4
US-09-764-864-389/c
; Sequence 389, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
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; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 389
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-389

Query Match      51.2%; Score 21; DB 10; Length 514;
Best Local Similarity 73.0%; Pred. No. 71;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      5 GCACCGAGCGCAGGCCCAACGGTCTGTGGGCCCCGAGCG 41
Db      453 GCACCGAGTGCCAGGACATCGAGCTGTGCCCGAGTG 417

RESULT 5
US-09-867-550-1483
; Sequence 1483, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and I
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-3113)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1483
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-550-1483

Query Match      51.2%; Score 21; DB 10; Length 569;
Best Local Similarity 73.0%; Pred. No. 71;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGTGGGCCCCG 37
Db      462 GGAGCCACCGAGCTTGGGGCCATCCATCTGGGGCCCTG 498

RESULT 6
US-09-859-101-2/c
; Sequence 2, Application US/09859101
; Patent No. US20020068825A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; Hillman, Jennifer L.
; Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN DBI/ACBP-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
```



```
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,101
; FILING DATE: 14-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,626
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0115 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1123 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: PGANNOT01
; CLONE: 620984
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-859-101-2
```

```
Query Match          51.2%; Score 21; DB 10; Length 1123;
. Best Local Similarity 73.0%; Pred. No. 71;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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```
Qy 4 GGCACCGAGCGCAGGCCCAACGGTCTGTGGCCCCGAGC 40
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 GGCTTGAGGCCTGGCCCAACCAAGTCTGTGGTCGCGAGC 22
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RESULT 7
US-10-098-841-134/c
; Sequence 134, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiachong B.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 134
; LENGTH: 1337
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (344)..(1192)
US-10-098-841-134

Query Match          51.2%; Score 21; DB 9; Length 1337;
. Best Local Similarity 73.0%; Pred. No. 71;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GGCACCGAGCGCAGGCCCAACGGTCTGTGGCCCCGAGC 40
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 281 GGCTTGAGGCCTGGCCCAACCAAGTCTGTGGTCGCGAGC 245

RESULT 8
US-09-864-761-5736/c
; Sequence 5736, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5736
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005849.1
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; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
US-09-864-761-5736

Query Match          50.7%; Score 20.8; DB 10; Length 457;
Best Local Similarity 70.0%; Pred. No. 82;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GGGGGCACCAGCGCAGGCCCAACGGTCTGGGCCCCGAGC 40
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Db 188 GCGGCCCCGGCGCGCAGGCCCCACGTGAGGGTCCAGGAAC 149

RESULT 9
US-10-006-950-1
; Sequence 1, Application US/10006950
; Patent No. US20020161216A1
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Bonini, James A.
; TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF4 RECEPTOR
; FILE REFERENCE: 58799
; CURRENT APPLICATION NUMBER: US/10/006,950
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: US/09/266,407
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 1
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-950-1

Query Match          50.7%; Score 20.8; DB 9; Length 1461;
Best Local Similarity 70.0%; Pred. No. 83;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GGGGGCACCAGCGCAGGCCCAACGGTCTGGGCCCCGAGC 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1410 GCGGCCCCGGCGCGCAGGCCCCACGTGAGGGTCCAGGAAC 1449

RESULT 10
US-09-805-467A-3
; Sequence 3, Application US/09805467A
; Patent No. US20020058259A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human Lipoxin A4
; TITLE OF INVENTION: Receptor-Like Protein
; FILE REFERENCE: 4974.00453
; CURRENT APPLICATION NUMBER: US/09/805,467A
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,037
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-805-467A-3

Query Match          50.7%; Score 20.8; DB 10; Length 2300;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy 1 GGGGGCACCAGCGCAGGCCCAACGGTCTGGGCCCCGAGC 40
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Db 1980 GCGGCCCCGGCGCGCAGGCCCCACGTGAGGGTCCAGGAAC 2019

RESULT 11
US-09-819-104A-3/c
; Sequence 3, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 7521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7521)
US-09-819-104A-3

Query Match          50.7%; Score 20.8; DB 9; Length 7521;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 GGGGCACCGAGCGCGCAGGCCCAACGGTCTGTGGCCCCGAGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4577 GGCTTACCCAGCTCAGGCACAATGACCGGGGCGCGCGCG 4538

RESULT 12
US-09-819-104A-1/c
; Sequence 1, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(7677)
US-09-819-104A-1

Query Match          50.7%; Score 20.8; DB 9; Length 8686;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 GGGGCACCGAGCGCGCAGGCCCAACGGTCTGTGGCCCCGAGCG 41
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Db 4733 GGCTTACCCAGCTCAGGCACAATGACCGGGGCGCGCGCG 4694

RESULT 13

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US-09-764-860-216
; Sequence 216, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-860-216

Query Match 50.2%; Score 20.6; DB 10; Length 239;
Best Local Similarity 74.3%; Pred. No. 96;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 GCACCGAGCGCAGGCCCAACGGTCTGGGCCCGGAG 39
||||||| ||||| ||| || |||||
Db 72 GCACCGAGGTCAGACCCAGAGGCCAGCGCCCGAG 106

RESULT 14

US-09-783-590-4787
; Sequence 4787, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4787
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (172)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (177)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (198)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (204)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (213)

; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (220)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (227)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (236)
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; NAME/KEY: misc feature
; LOCATION: (243)
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; LOCATION: (246)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (278)
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; NAME/KEY: misc feature
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (304)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (307)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (346)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (347)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (358)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-4787
Query Match 50.2%; Score 20.6; DB 10; Length 366;
Best Local Similarity 74.3%; Pred. No. 96;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 5 GCACCGAGCGCAGGCCCAACGGTCTGGGCCCGGAG 39
||||||| ||||| ||| || |||||
Db 72 GCACCGAGGTCAGACCCAGAGGCCAGCGCCCGAG 106
RESULT 15
US-10-026-188-6/c
; Sequence 6, Application US/10026188
; Patent No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 155074
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human genomic region containing ltrpc5
; OTHER INFORMATION: (Human Chromosome 11p15.5 PAC clone pDJ915f1
; OTHER INFORMATION: containing KvLQT1 gene)

US-10-026-188-6

Query Match 50.2%; Score 20.6; DB 9; Length 155074;
Best Local Similarity 74.3%; Pred. No. 1e+02;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 6 CACCGAGCGCAGGCCCAACGGTCTGGGCCCGAGC 40
| | | | | | | | | | | | | | | | | |
Db 51942 CTCCAGCCCAAGACCCAGGGTCTCGGCCAGTGC 51908

Search completed: March 11, 2003, 23:15:29
Job time : 79.1538 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:30:36 ; Search time 23887.5 Seconds
(without alignments)
915.286 Million cell updates/sec

Title: US-09-636-259C-1
Perfect score: 1350
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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				7:	em_estro:*		
				8:	em_htc:*		
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				16:	em_estom:*		
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				23:	em_gss_mam:*		
				24:	em_gss_mus:*		
				25:	em_gss_other:*		
				26:	em_gss_pro:*		
				27:	em_gss_rod:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

C 1	561	41.6	561	14 BM967248	BM967248 iJ32d04.Y
C 2	490.4	36.3	492	14 BM967243	BM967243 iJ32c09.Y
C 3	479	35.5	691	10 BB643669	BB643669 BB643669
C 4	453	33.6	453	14 BQ129312	BQ129312 iJ34d05.Y
5	410.6	30.4	893	13 BI459381	BI459381 603200147
6	395	29.3	740	13 BI838282	BI838282 603083213

	7	364.8	27.0	1077	9	AL544609	AL544609
	8	320.2	23.7	855	17	GGAA2AAR	AL606540 Chicken a
C	9	319.4	23.7	358	13	BM352981	BM352981 ig69h02.y
	10	317.6	23.5	867	9	AL530418	AL530418 AL530418
	11	317.4	23.5	988	14	BQ887729	BQ887729 AGENCOURT
	12	272.6	20.2	297	14	BQ302172	BQ302172 QV0-BT026
	13	255.2	18.9	935	14	BQ923710	BQ923710 AGENCOURT
	14	226.4	16.8	896	17	CNS03BQW	AL236849 Tetraodon
	15	214.6	15.9	966	17	CNS02NV2	AL205895 Tetraodon
C	16	199.8	14.8	1135	9	AL544577	AL544577 AL544577
C	17	197	14.6	805	17	CNS03CEL	AL237702 Tetraodon
	18	194.2	14.4	350	10	BE648878	BE648878 UI-M-BH2.
	19	185.8	13.8	777	17	LREA2AR	AL606561 Lamprey a
	20	185.6	13.7	801	17	GGAA2CAR	AL606541 Chicken a
	21	179.4	13.3	1010	17	CNS04CMQ	AL284651 Tetraodon
	22	177.2	13.1	702	13	BI836679	BI836679 603089610
	23	176.6	13.1	975	17	CNS03RV	AL234292 Tetraodon
	24	175.8	13.0	921	17	CCLA2BAR	AL606559 Herring a
	25	173.4	12.8	691	17	HIPA2AAR	AL606565 Sea Horse
	26	172.6	12.8	774	17	AGAA2C2AR	AL606580 Toothcarp
	27	172.2	12.8	882	17	HIPA2C2AR	AL606568 Sea Horse
	28	171.4	12.7	697	17	RESA2AAR	AL606551 Frog alph
	29	170.6	12.6	2146	11	AK018378	AK018378 Mus muscu
	30	169.6	12.6	872	17	ECAA2BAR	AL606560 Horse alp
	31	167.8	12.4	825	17	ARUA2BAR	AL606576 Sturgeon
C	32	166.8	12.4	890	17	CNS02WK9	AL217170 Tetraodon
	33	164.8	12.2	693	17	ARUA2AAR	AL606574 Sturgeon
	34	164	12.1	535	13	BM647571	BM647571 170006873
	35	163.4	12.1	723	17	AGAA2A2AR	AL606581 Toothcarp
	36	161.8	12.0	829	9	AL549866	AL549866 AL549866
	37	160.6	11.9	705	17	HGRA2AAR	AL606570 Shark alp
	38	160	11.9	753	17	SCAA2CAR	AL606564 Ostrich a
	39	159.4	11.8	788	17	DREA2CAR	AL606584 Zebrafish
	40	158.6	11.7	699	17	LOSA2AAR	AL606553 Gar alpha
	41	154.4	11.4	981	17	HIPA2BAR	AL606569 Sea Horse
C	42	151.4	11.2	872	9	AL573897	AL573897 AL573897
	43	151	860	17	CNS03HKQ	AL244403 Tetraodon	
	44	148.8	11.0	780	17	CCLA2CAR	AL606557 Herring a
45	148	11.0	984	9	AL550664	AL550664 AL550664	

ALIGNMENTS

RESULT 1
BM967248/c
LOCUS BM967248 561 bp mRNA linear EST 29-APR-2002
DEFINITION iJ32d04.Y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
CDNA clone IMAGE:6136374 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.

ACCESSION BM967248
VERSION BM967248.1 GI:19561047
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
Other_ESTs: iJ32d04.x1

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other_ESTs: iJ32d04.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812

Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 445.

FEATURES
source
Location/Qualifiers
1. .561
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136374"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 63 a 215 c 210 g 73 t
ORIGIN

Query Match 41.6%; Score 561; DB 14; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.8e-92;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 TCCTTCTTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGCGCATCTACCAGATCGCC 669
|||||
Db 561 TCCTTCTTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGCGCATCTACCAGATCGCC 502
|||||

QY 670 AAGCGTCGACCCCGCTGCCACCCAGCCGCGGGTCCGGACGCCGCTCGCCGCGCCGCG 729
|||||
Db 501 AAGCGTCGACCCCGCTGCCACCCAGCCGCGGGTCCGGACGCCGCTCGCCGCGCCGCG 442
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QY 730 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCGCAGCGCGGGCCCCGGGGGC 789
|||||
Db 441 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCGCAGCGCGGGCCCCGGGGGC 382
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QY 790 GCAGAGGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGCCCGCGCCGCGCC 849
|||||
Db 381 GCAGAGGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGCCCGCGCCGCGCC 322
|||||

QY 850 GGGCCGCGCGACACCGACGCGCTGGACCTGGAGGAGAGCTCGTCTTCGACCCACGCCGAG 909
|||||
Db 321 GGGCCGCGCGACACCGACGCGCTGGACCTGGAGGAGAGCTCGTCTTCGACCCACGCCGAG 262
|||||

QY 910 CGGCCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCGGGGCAAGGCAAGGCCCGCGAGCG 969
|||||
Db 261 CGGCCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCGGGGCAAGGCAAGGCCCGCGAGCG 202
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QY 970 AGCCAGGTGAAGCCGGCGACAGCCTGCCGCGCGCGGGCGCGGGGCGACGGGGATCGGG 1029
|||||
Db 201 AGCCAGGTGAAGCCGGCGACAGCCTGCCGCGCGCGGGCGCGGGGCGACGGGGATCGGG 142
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QY 1030 ACGCCGGCTGCAGGGCCGGGGAGGAGCGCGTCCGGGGCTGCCAAGGCGTCGCGTGGCGC 1089
|||||
Db 141 ACGCCGGCTGCAGGGCCGGGGAGGAGCGCGTCCGGGGCTGCCAAGGCGTCGCGTGGCGC 82
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QY 1090 GGGCGGCAGAACCGCGAGAACGGCTTACGTTCTGTGCTGGCCGTGGTTCATCGGAGTGTC 1149
|||||

Db 81 GGGCGGCAGAACCGCGAGAACGCTTCACGTCGTGCTGGCCGTGTCATCGGAGTGTC 22
|||||

QY 1150 GTGGTGTGCTGGTTCCTTC 1170
|||||

Db 21 GTGGTGTGCTGGTTCCTTC 1
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RESULT 2
BM967243/c
LOCUS
DEFINITION
BM967243 492 bp mRNA linear EST 29-APR-2002
ij32c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6136336 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BM967243
BM967243.1 GI:19561038
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 492)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Tsagataishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: ij32c09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 455.

FEATURES
source
Location/Qualifiers
1. .492
/organism="Homo sapiens"
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/clone="IMAGE:6136336"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 44 a 202 c 182 g 64 t
ORIGIN

Query Match 36.3%; Score 490.4; DB 14; Length 492;
Best Local Similarity 99.8%; Pred. No. 1.8e-79;
Matches 491; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 679 ACCCGGTGCCACCCAGCCCGCGGGTCCGAGCCCGTCGCCCGCGCGCGGGGGCACC 738
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QY 739 GAGCGAGGCCCAACGGTCTGGGCCCCGAGCGCAGCGCGGCCCGGGCGCAGAGGCC 798
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Db 432 GAGCGAGGCCCAACGGTCTGGGCCCCGAGCGCAGCGCGGCCCGGGCGCAGAGGCC 373
|||||

QY 799 GAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGCCCCGCGCGCGCGCGCGC 858
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Db 372 GAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGCCCCGCGCGCGCGCGCGC 313
|||||

QY 859 GACACCGACCGCTGGACCTGGAGGAGTCTGCTTCCGACCAACCGCAGCGGCCTCCA 918
|||||
Db 312 GACACCGACCGCTGGACCTGGAGGAGTCTGCTTCCGACCAACCGCAGCGGCCTCCA 253
|||||

QY 919 GGGCCCCGACCCGAGCGCGTCCCCGGGGCAAGGCAAGCCCCGAGCGCAGGTG 978
|||||
Db 252 GGGCCCCGACCCGAGCGCGTCCCCGGGGCAAGGCAAGCCCCGAGCGCAGGTG 193
|||||

QY 979 AAGCCGGCGACAGCTGCCGCGCGCGCGGGCGCGACGGGATCGGACGCCGGCT 1038
|||||
Db 192 AAGCCGGCGACAGCTGCCGCGCGCGCGGGCGCGACGGGATCGGACGCCGGCT 133
|||||

QY 1039 GCAGGGCCGGGGAGGAGCGCTCGGGGCTGCCAAGGCGTCGCGCTGGCGCGGGCGCAG 1098
|||||
Db 132 GCAGGGCCGGGGAGGAGCGCTCGGGGCTGCCAAGGCGTCGCGCTGGCGCGGGCGCAG 73
|||||

QY 1099 AACC CGAGAGCGCTTACGTTCTGCTGCGCGGTGGTCAATCGGAGTGTTCGTGTGTC 1158
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Db 72 AACC CGAGAGAGCGCTTACGTTCTGCTGCGCGGTGGTCAATCGGAGTGTTCGTGTGTA 13
|||||

QY 1159 TGGTTCCTTC 1170
|||||
Db 12 TGGTTCCTTC 1

RESULT 3
BB643669/c
LOCUS BB643669 691 bp mRNA linear EST 26-OCT-2001
DEFINITION BB643669 RIKEN full-length enriched, adult male corpora
quadrigemina Mus musculus cDNA clone B230352011 5', mRNA sequence.
ACCESSION BB643669
VERSION BB643669.1 GI:16478370
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 691)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
Location/Qualifiers
1. .691
/organism="Mus musculus"
/db xref="taxon:10090"
/clone="B230352011"
/clone_lib="RIKEN full-length enriched, adult male corpora
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/lab_host="DH10B"
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCACAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTCGATTAAATTAATATCCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."
BASE COUNT 158 a 182 c 233 g 118 t
ORIGIN
Query Match 35.5%; Score 479; DB 10; Length 691;
Best Local Similarity 87.5%; Pred. No. 2.2e-77;
Matches 547; Conservative 0; Mismatches 75; Indels 3; Gaps 2;
QY 1 ATGGGCTCCCTGACCGGACCGGGCAACCGAGCTGGAACGGGACCGCGCGGGG 60
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Db 623 ATGGGCTCCCTCCAGCGGAATGCGGCCACAGC-AGCTGGAACGGGACCAAGCGCCGGAG 565
|||||
QY 61 GGCGGGCGCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCTGGCC 120
| | | | |
Db 564 G-CGGCACCCAGCCCCCTTACTCCCTGCAGGTGACACTGACGCTGGTGTGCTGGCT 507
| | | | |
QY 121 GGCCTGCTCATGCTCACCCTGTTTCGGCAACGTGCTCGTCATCATCGCCGTGTTACG 180
| | | | |
Db 506 GGCCTGCTCATGCTGTTACAGTATTTGGCAACGTGCTGGTTATTATCGGGTGTTCACC 447
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QY 181 AGCCGGCGGCTCAAGCGGCCCCCAAAACCTCTCTCTGGTGTCTCTGGCCTCGGCCGACATC 240
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Db 446 AGTCGGCGCTCAAGACTCCCCAAACCTTCTCCTGGTGTCCCTGGCCTCAGCGGACATC 387
QY 241 CTGGTGGCCACGCTCGTCATCCCTTTCTCGCTGGCCAAACGAGGTACATGGGTACT 300
Db 386 CTGGTGGCCACGCTGGTCATTCCTTTTCTTTGGCCAAACGAGGTATGGTTACTGGTAC 327
QY 301 TTCGGCAAGGCTTGTGCGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCGTCC 360
Db 326 TTTGGTAAGGTGTGTGTGAGATCTATTGGCTCTCGACGTGCTCTTTTGACAGTCGTCC 267
QY 361 ATCGTGCACCTGTGCGCCATCAGCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAG 420
Db 266 ATAGTGACCTGTGGCCATCAGCCTTGACCGCTACTGGTCCATCAGCAGGCCATCGAG 207
QY 421 TACAACTGAAGCGACCGCGCGCATCAAGGCCATCATCATCACCTGCTGGGTCTATC 480
Db 206 TACAACTGAAGCGACCGCGCGTTCGCATCAAGGCCATCATTTGTACCGTGTGGGTCTATC 147
QY 481 TCGGCGGTATCTCTCTCCCGCGCTCATCTCCATCGAGAAAGCGCGCGCGCGC 540
Db 146 TCGGCTGTATCTCTCTCCCGCACTCATCTCCATAGAGAAGAGGCGCTGGCGCGGG 87
QY 541 CCGCAGCGCGCGCGCTGCGAGATCAACGACCAAGTGGTACGTCTATCTCGTCG 600
Db 86 CAGCAGCGCGCGCGCAAGCTGCAAGATCAACGACCAAGTGGTATGTCTATCTCCTCG 27
QY 601 TGCATCGGCTCCTTCTTCGCTCCCT 625
Db 26 TCCATCGGTTCTTCTTCGCGCCTT 2

RESULT 4
BQ129312/c
LOCUS
DEFINITION
iJ34d05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6136736 5', similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
ACCESSION
BQ129312
VERSION
BQ129312.1 GI:20203223
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 453)
AUTHORS
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: iJ34d05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohpc.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .453
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/db_xref="taxon:9606"
/clone="IMAGE:6136736"

FEATURES
source
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/sex="Both"
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/dev_stage="Adult"
/lab_host="DH10B"
/notes="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
BASE COUNT 41 a 189 c 164 g 59 t
ORIGIN
Query Match 33.6%; Score 453; DB 14; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e-72;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 718 GCCGCGCGCGCGGGCACCGAGCGCAGGCCCCAACGGTCTGGGCCCCGAGCGCAGCGC 777
Db 453 GCCGCGCGCGCGGGGGCACCGAGCGCAGGCCCCAACGGTCTGGGCCCCGAGCGCAGCGC 394
QY 778 GGCCCCGGGGGGCGAGAGGGCCGAACCGCTGCCCCACCCAGCTCAACGGCGCCCCCTGGCGAG 837
Db 393 GGCCCCGGGGGGCGAGAGGGCCGAACCGCTGCCCCACCCAGCTCAACGGCGCCCCCTGGCGAG 334
QY 838 CCCGCGCGCGCGGGCGCGGACACCGACCGCGCTGGACCTGGAGGAGAGCTCGTCTTCC 897
Db 333 CCCGCGCGCGCGGGCGCGGACACCGACCGCGCTGGACCTGGAGGAGAGCTCGTCTTCC 274
QY 898 GACCACGCCGAGCGGCTCCAGGGCCCCCGCAGACCCGAGCGCGGTCCCCGGGGCAAAGGC 957
Db 273 GACCACGCCGAGCGGCTCCAGGGCCCCCGCAGACCCGAGCGCGGTCCCCGGGGCAAAGGC 214
QY 958 AAGGCCCCGAGCGAGCCAGGTGAAGCCGGGCGACAGCCTGCCGCGCGCGGCGCGGGGCG 1017
Db 213 AAGGCCCCGAGCGAGCCAGGTGAAGCCGGGCGACAGCCTGCCGCGCGCGGCGCGGGGCG 154
QY 1018 ACGGGGATCGGGACCGCGGTGCAGGGCCGGGGGAGGAGCGCGTCGGGGCTGCCAAGGCG 1077
Db 153 ACGGGGATCGGGACCGCGGTGCAGGGCCGGGGGAGGAGCGCGTCGGGGCTGCCAAGGCG 94
QY 1078 TCGCGTGGCGCGCGGGCAGAACCCGCGAGAACGCTTCACGTTTCGTGCTGGCCGTGGTC 1137
Db 93 TCGCGTGGCGCGGGCGGCAGAACCCGCGAGAACGCTTCACGTTTCGTGCTGGCCGTGGTC 34
QY 1138 ATCGGAGTGTTCGTGTGTGCTGGTTCCCTTC 1170
Db 33 ATCGGAGTGTTCGTGTGTGCTGGTTCCCTTC 1

RESULT 5
BI459381
LOCUS
DEFINITION
603200147F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266354 5',
mRNA sequence.
ACCESSION
BI459381
VERSION
BI459381.1 GI:15250037
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 893)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
```


TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11671 row: m column: 11
High quality sequence stop: 716.
Location/Qualifiers
1. .893
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/clone="IMAGE:5266354"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 149 a 303 c 290 g 151 t
ORIGIN
Query Match 30.4%; Score 410.6; DB 13; Length 893;
Best Local Similarity 86.0%; Pred. No. 6.le-65;
Matches 586; Conservative 0; Mismatches 74; Indels 21; Gaps 11;
QY 1 ATGGGCTCCCTGCAGCCGGACCGGGCAACGCGAGCTGGAACGGACCGAGCGCGGG 60
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213 ATGGGCTCCCTGCAGCCGGACCGGGCAACGCGAGCTGGAACGGACCGAGCGCGGG 272
QY 61 GGCGGCGCGCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
273 GGCGGCGCGCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCC 332
QY 121 GGCCTGCTCATGCTGCTCACCGTGTTCCGCAACGCTGCTCGTCATCATCGCCGTTCACG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
333 GGCCTGCTCATGCTGCTCACCGTGTTCCGCAACGCTGCTCGTCATCATCGCCGTTCACG 392
QY 181 AGCCGCGCGTCAAGGCGCGCCCAAAACCTCTTCTGGTGCTCTGG--CCTCGGCGGACA 238
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
393 AGCCGCGCGTCAAGGCGCGCCCAAGACTCTTCTGGTGCTCTGGACCTCGGACGAAAT 452
QY 239 TCCTGGTGGCACGCTCGT-CATCCCTTTCTCGCTGGCCAACGAGGTGATGGCTACTGG 297
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
453 TCCTGGTGGCCACGCTCGTACATCCCTTTCTCGCTGGCCAACGAGGTGATGGCTACTGG 512
QY 298 TACTTCGGCAA-GGCTTGGTGG-AGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGT 355
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
513 TACTTCGGCAAGGGCTTGGTGCGAAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGT 572
QY 356 -CGTCCATCGTGACCTGTGCGCCATCAGCCTGGACCGGTACTGGTCCATCACACAGGCC 414
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
573 ACGTCCATCGTGACCTGTGCGCCATCAGCCTGGACCGGTACTGGTCCATCACACAGGCC 632
QY 415 ATCGAGTACAACCTGAAGCGCACGCCGCGCGCATCAAGGCCATCATCACCGGTGG 474
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
633 ATCGAGTACAACCTGAAGCGCACGCCGCGCGCATCAAGGCCATCATCACCGGTGG 692
QY 475 GTC-ATCTCGGCGGTCACTCTCTCCCG-----CCGCTCATCTCCATCGAGAAGAGG 526
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693 GTCAATCTCGGCGTCAGTCTCTCTTCCCGCGGTTTCATCTCCACTCGGAGAACACGGG 752

QY 527 GCGGCGGCGGCGGCC--GCAGCCGGCCGAGCCGCGTGCAGATCAACGA--CCAGAAGT 583
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
753 CGGAGGAGGCGGCCAGGAAGCGGCCGAGCCCGCGGAAGAATCACGACGCAGAAAGG 812
QY 584 GGTACGTATCTCGTCGTG---CATCGGCTCCTTCTTCGTCCTCCCTCATCATGATCC 640
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 641 TGGTCTACGTGCGCATCTACC 661
Db ||||| ||||| ||||| |||||
873 TGG-CAACGCGCGCATATACC 892
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BI838282
LOCUS BI838282 740 bp mRNA linear EST 04-OCT-2001
DEFINITION 603083213F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222475 5', mRNA sequence.
ACCESSION BI838282
VERSION BI838282.1 GI:15949832
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11559 row: i column: 04
High quality sequence stop: 740.
Location/Qualifiers
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/clone="IMAGE:5222475"
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Best Local Similarity 100.0%; Pred. No. 4e-62;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 956 GCAAGGCCGAGCGAGCCAGGTGAAGCCGGCGACAGCCTGCCGCGCGCGCGGGG 1015
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1 GCAAGGCCGAGCGAGCCAGGTGAAGCCGGCGACAGCCTGCCGCGCGCGCGGGG 60
QY 1016 CGACGGGGATCGGACCGCGGCTGCAGGGCCGGGGAGGAGCGCGTCCGGGCTGCCAAG 1075
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61 CGACGGGGATCGGACCGCGGCTGCAGGGCCGGGGAGGAGCGCGTCCGGGCTGCCAAG 120
QY 1076 CGTCGCGCTGGCGGGCGGAGAACCCGAGAACGCTTCACGTTCTGTCGCGCGTGG 1135
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QY 527 GCGGCGGCGGCGGCC--GCAGCCGGCCGAGCCGCGTGCAGATCAACGA--CCAGAAGT 583
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753 CGGAGGAGGCGGCCAGGAAGCGGCCGAGCCCGCGGAAGAATCACGACGCAGAAAGG 812
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QY 641 TGGTCTACGTGCGCATCTACC 661
Db ||||| ||||| ||||| |||||
873 TGG-CAACGCGCGCATATACC 892
RESULT 6
BI838282
LOCUS BI838282 740 bp mRNA linear EST 04-OCT-2001
DEFINITION 603083213F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222475 5', mRNA sequence.
ACCESSION BI838282
VERSION BI838282.1 GI:15949832
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11559 row: i column: 04
High quality sequence stop: 740.
Location/Qualifiers
1. .740
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5222475"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

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QY 466 ACCGTGTGGGTTCATCTCGGCCGTTCATCTCCTTCCCGCCGCTCATCTCCATCGAGAAG 525
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QY 526 GGCGGGCGGGCGCGCAGCCGCGGAGCGCGGCTGCGAGATCAACGACCAGAAGTGG 585
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QY 586 TACGTTCATCTCGTCGTGCATCGGTCCTTCTTTCGCTCCCTGCTTCATCATGATCCTGGTC 645
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Db 454 AAGGAGGACCTG-----CCTGCCTCAGCCCGAGCTCAATGGAGAGA 493
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LOCUS
DEFINITION ig69h02.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:A2AA_HUMAN
P08913 ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
ACCESSION BM352981
VERSION BM352981.1 GI:18085339
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 358)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,B., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
, Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: ig69h02.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 342.
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1..358
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/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
BASE COUNT 76 a 114 c 115 g 53 t
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Query Match 23.7%; Score 319.4; DB 13; Length 358;
Best Local Similarity 99.7%; Pred. No. 2e-48;
Matches 320; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 58 TCGGGGGACAGGAAGGGAT 38
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LOCUS prime, mRNA sequence. CS0DD007YE02 5
DEFINITION
ACCESSION AL530418
VERSION AL530418.1 GI:12793911
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/clone="CS0DD007YE02"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 98 a 315 c 286 g 143 t 25 others
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Query Match 23.5%; Score 317.6; DB 9; Length 867;
Best Local Similarity 76.8%; Pred. No. 4.7e-48;
Matches 407; Conservative 8; Mismatches 102; Indels 13; Gaps 2;
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Db 590 GTTTTGCACCTCGTCGATCGTGATCTGTGTKCAAACAGCCTGGACCGCTACTGGKCGGT 649
QY 405 CACACAGGCCATCGAGTACAACTGAAGCGCACGCCCGCGCATCAAGGCCATCATCAT 464
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LOCUS AGENCOURT 8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
DEFINITION 5', mRNA sequence.
ACCESSION BQ887729
VERSION BQ887729.1 GI:22279743
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 988)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13739 row: m column: 06
High quality sequence start: 8
High quality sequence stop: 509.
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Location/Qualifiers
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/clone="IMAGE:6313133"
/clone_lib="NIH_MGC_129"
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unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
is a NIH MGC Library."
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Query Match 23.5%; Score 317.4; DB 14; Length 988;
Best Local Similarity 74.4%; Pred. No. 5.2e-48;
Matches 432; Conservative 0; Mismatches 136; Indels 13; Gaps 2;
QY 169 GCCGTGTTACGAGCCGCGCTCAAGGCGCCCCAAAACCTTCTCCTGGTGTCTCTGGCC 228
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Db 19 GCTGTGTTGACCAAGCCGAGCACTGCGCGCCCGCAGAACCTCTTCTCGTGTCTCTGGCC 78
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LOCUS BQ302172 297 bp mRNA linear EST 16-MAY-2002
DEFINITION QV0-BT0263-101299-072-h10 BT0263 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ302172
VERSION BQ302172.1 GI:20817694
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 297)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV0&t2=QV0-BT0263-
101299-072-h10&t3=1999-12-10&t4=1)
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Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 40 a 109 c 91 g 57 t
ORIGIN
Query Match 20.2%; Score 272.6; DB 14; Length 297;
Best Local Similarity 98.6%; Pred. No. 6.1e-40;
Matches 275; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ATGGGCTCCCTGCAGCGGACGCGGCAACGCGAGCTGGAACGGGACCGAGCGCGGG 60
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Db 11 ATAGGCTCCCTGCAGCGGACGCGGCAACGCGAGCTGGAACGGGACCGAGCGCGGG 70
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QY 121 GGCCTGCTCATGCTCATCCGCTGTTCCGGCAACGTCGTCATCATCGCCGTGTTACG 180
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QY 181 AGCCGCGCGCTCAAGCGCGCCCCAAACCTTCTCCTGGTGTCTCTGGCCTCGGCCGACATC 240
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Db 191 AGCCGCGCGCTCAAGCGGCTCCAAACCTTCTCCTGGTGTCTCTGGCCTCGGCCGACATC 250
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Db 251 CTGGTGGCCACGCTCGTCATCCCTTCTCGCTGGCCCTAC 289
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BQ923710
LOCUS BQ923710 935 bp mRNA linear EST 20-AUG-2002
DEFINITION AGENCOURT_88032111 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6198830 5', mRNA sequence.
ACCESSION BQ923710
VERSION BQ923710.1 GI:22338741
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13611 row: b column: 15
High quality sequence stop: 535.
FEATURES
Location/Qualifiers
1..935
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6198830"
/clone_lib="Lupski_sciatic_nerve"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.

Directionally cloned using the following adaptors:

5'-TCGACCCACGGTCCG-3' and
5'-GACTAGTTCTAGATCGGAGCGCGCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Iupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT 130 a 343 c 278 g 184 t
ORIGIN

Query Match 18.9%; Score 255.2; DB 14; Length 935;
Best Local Similarity 96.6%; Pred. No. 1e-36;
Matches 282; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 1 ATGGGCTCCCTGACCGGACGCGGGCAACGCGAGCTGGAACGGACCGAGGCGCGGG 60
|||||
Db 394 ATGGGCTCCCTGACCGGACGCGGGCAACGCGAGCTGGAACGGACCGAGGCGCGGG 453
|||||
QY 61 GCGGGCGCGCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCC 120
|||||
Db 454 GCGGGCGCGCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCC 513
|||||
QY 121 GGCCTGCTCATGTGCTCACCGTGTTCGGCAACGTGCTCGTCAATCATGCCGTGTTACG 180
|||||
Db 514 GGCCTGCTCATGTGCTCACCGTGTTCGGCAACGTGCTCGTCAATCATGCCGTGTTACG 573
|||||
QY 181 AGCCGCGCGCTCAAGCGGCCCAAAACCTCTCTGTTGTTCTCTGGCC-TCGGCCGACAT 239
|||||
Db 574 AGCCGCGCGCTCAAGCGGCCCAAAACCTCTCTGTTGTTCTCTGGCC-TCGGCCGACAT 633
|||||
QY 240 CCTGGTGGCCACGCTCGTCAATCCC-TTTCTCGCTGGCCAACGAGGTCAATGG 290
|||||
Db 634 CCTGGTGGCCACGCTCGTCAATCCC-TTTCTCGCTGGCCAACGAGGCTTGG 685
|||||

RESULT 14
CNS03BQW
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
012P03 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL236849
AL236849.1 GI:7895984
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS
1 (bases 1 to 896)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence

TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 896)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.

TITLE
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished
3 (bases 1 to 896)
Genoscope.
Direct Submission
Submitted (12-APR-2000)

This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
Location/Qualifiers
1. .896
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="012P03"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG012CH02SP1-end :
PUC-Ori"

BASE COUNT 163 a 276 c 295 g 157 t 5 others
ORIGIN

Query Match 16.8%; Score 226.4; DB 17; Length 896;
Best Local Similarity 75.1%; Pred. No. 1.7e-31;
Matches 281; Conservative 1; Mismatches 92; Indels 0; Gaps 0;

QY 82 TACTCCCTGACGTGACGCTGACGCTGGTGTGCTGGCGGCTGCTCATGCTGCTCACC 141
|||||
Db 498 TACTCCTTAGGGGCCACCGCCGGCATCCCGCGCTCGTCAGCTTCCTCATCCTGTTACG 557
|||||
QY 142 GTGTTTCGGCAACGTGCTCGTCAATATCGCCGTGTTTCACGAGCCGCGCTCAAGGGCCCC 201
|||||
Db 558 GTGGTCGGGAACATCCTGGTGGTGGTGGCGGTGCTGACGAGCCGCGCTCAGAGCGCCG 617
|||||
QY 202 CAAAACCTCTTCCTGGTGTCTCTGGCCTCGGCCCGACATCCTGTGGCCACGCTCGTCATC 261
|||||
Db 618 CAGAACCTCTTCCTGGTGTCTCTGGCCACCGCGGACATCCTGTGGCCACCCCTGGTGATG 677
|||||
QY 262 CCTTTCTCGCTGGCCAAACGAGGTCAATGGCTACTGGTACTTTCGCAAGGCTTGGTGGAG 321
|||||
Db 678 CCCTTCTCCCTGGCCAAACGAACTGATGGCTACTGGTATTTTCGCGAGAGTCTGGTGGGG 737
|||||
QY 322 ATCTACCTGGCGCTCGACGTGCTCTTCTGCACGCTCGTCCATCGTGACCTGTGCGCCATC 381
|||||
Db 738 ATTATCTGGCTCTGGATGTTTATTCTTGCACTCGTCGATCGTCCATCTGTGCGCAATA 797
|||||
QY 382 AGCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTACACCTGAAGCGCACGCCG 441
|||||
Db 798 AGCTTGGACCGCTACTGGTCTGTACAGCGCGGTCCAGTACAACTGAAGAGGACCCCT 857
|||||

RESULT 15
CNS02NV2
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
152E12 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL205895
AL205895.1 GI:7864714
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 966)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.

TITLE
JOURNAL
REFERENCE
AUTHORS
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 966)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.

TITLE
JOURNAL
COMMENT
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished

REFERENCE	3 (bases 1 to 966)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES	Location/Qualifiers
source	1..966 /organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone="152E12" /clone_lib="G" /note="Genoscope sequence ID : C0AG152BC06LP1-end : T7"
BASE COUNT	197 a 283 c 303 g 175 t 8 others
ORIGIN	
Query Match	15.9%; Score 214.6; DB 17; Length 966;
Best Local Similarity	75.5%; Pred. No. 2.4e-29;
Matches 265; Conservative 1; Mismatches 85; Indels 0; Gaps 0;	
QY	82 TACTCCCTGCAGGTGACGGTGACCGTGGTGTCCTGGCCGCCGCTCATGCTGTCAACC 141
Dd	608 TACTCCTTAGGGCYACCGCCGGCATCGCCGGCTCGTTAGTTCCTCATCCTGTTCACG 667
QY	142 GTGTTCGGCAACGTGCTCGTCATCATCGCCGTTTCACGAGCGCGCGCTCAAAGCGCCC 201
Dd	668 GTGGTCGGGAACATCCTGGTGGTGCTCGGGTGCTGACGAGCGCGCGCTCAGAGCGCG 727
QY	202 CAAAACCTCTTCTGGTGCTCTGGCCTCGGCCGACATCCTGTGGCCACGCTCGTCAAC 261
Dd	728 CAGAACCTCTTCTGGTGCTCTGGCCACCGCGGACATCCTGGTCGCCACCCCTGGTGATG 787
QY	262 CCTTTCTCGCTGGCCAACGAGGTGATGGGCTACTGGTACTTCGGCAAGGCTTGGTGGAG 321
Dd	788 CCCTTCTCCCTGGCCAACGAACTGATGGGCTACTGGTATTTCGGCAGAGTCTGGTGGGG 847
QY	322 ATCTACCTGGCGCTCGACGTGCTTCTGACGTCGTCCAATCGTGCAACCTGTGCGCCATC 381
Dd	848 ATTATCTGGCTCTGGATGTTTTATTCTGCACCTCGTCGATCGTCCATCTGTGCGCAATA 907
QY	382 AGCTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTACAACCTGAAG 432
Dd	908 AGCTTGGACCGCTACTGGTCTGTGACGCGAGCGGTCAGTACAACCTGAAR 958

Search completed: March 11, 2003, 07:39:11
Job time : 23901.5 secs

Db 195 CATCCCTTTCTCGCTGGCCAACGAGCTGCTGGGCTACTGGTACTTCCGGCGCACGTTGGTG 254

QY 318 CGAGATCTACCTGGCGCTCGACGTGCTCTTCTTGCCACGTCGTCCATCGTGCACCTGTGCGC 377

Db 255 CGAGGTGTACCTGGCGCTCGACGTGCTCTTCTGCACCTCGTCCATCGTGCACCTGTGCGC 314

QY 378 CATCAGCCTGGACCGGTACTGGTCCATCACACAGGCCCATCGAGTACAACTGAAGCGCAC 437

Db 315 CATCAGCCTGGACCGGTACTGGCCGTGAGCCGCGCTGGAGTACAACTCCAAGCGCAC 374

QY 438 GCCGCGCGCATCAAGGCCCATCATCATCACCGTGTGGGTATCTCGGCCGTATCTCCTT 497

Db 375 CCCGCGCGCATCAAGTGCATCATCTCACTGTGTGGTCTATCGCCGCGTCACTCTCGCT 434

QY 498 CCCGCGCGTCATCTCCATCGAGAAAGAGGGCGGGCGGGCGGCCCGAGCCCGCGAGCC 557

Db 435 GCCGCCCCCTCATCT-----ACAAGGGCGACAGGGCCCCCAGCGCGCGGGCGCCC 485

QY 558 GCGCTGCGAGATCAACGACCAGAAAGTGTACGTATCTCTCGTGTGATCGGCTCCTTCTT 617

Db 486 CCAGTGAAGCTCAACGAGAGCCCTGGTATACCTCTGGCCTCCAGCATCGGATCTTCTT 545

QY 618 CGCTCCCTGCCTCATCATGATCCTGGTCTACGTGCGCATCTACCAGATCGCCAAAGCGTCG 677

Db 546 TGCTCCTTGCCTCATCATGATCCTTGTCTACCTGCGCATCTACCTGTATCGCCAAACGCAG 605

QY 678 CACCCGCGTGCACCCA-----GCGCGCGGGTCCGGACGCCGTCTG 718

Db 606 CAACCGCAGAGGTCCAGGGCCAAAGGGGGGCGCTGGGCAGGGTGAGTCCAAGCAGCCCCG 665

QY 719 CCGCGCCCGCGGGGGACCGAGCGCAGGCCCAACGGTCTGGGC----- 763

Db 666 ACCGACCATGTTGGGGCTTTGGCCCTCAGCCAACTGCCAGCCCTGGCCCTCTGTGGCTTC 725

QY 764 -----CCGAGCGCAGCGCGGGCCCGGGGGCGCAGAGGCCGAAACCGCTGCCAC 812

Db 726 TGCCAGAGAGGTCAACGGACACTCGAAGTCCACTGGGGAGAAGGAGGGGAGACCCC 785

QY 813 CCAGCTCAACGGCGCCCTGGCGAGCCCGCGCGCGGGCGCGCGACACCGACGCGCT 872

Db 786 TGAAGATACTGGGACCCCGGCGCTTGCCACCCAGTTGGGCTGCCCTTCCCAACTCAGGCCA 845

QY 932 GGACCTGGAGGAGCTCGTCTTCGACCAACGCGCGAGCGGCTCCAGGGCCCGCAGACC 932

Db 846 GGGCAGAAAGGAGGTGTTTGTGGGCACTCTCCAGAGGATGAAGTGAAGAGGAGGAAGA 905

QY 933 CGAGCGCGGTCCCCGGGGCAAGCAAGGCCCGAGCGGACGAGTGAAGCCGGCGCAGAG 992

Db 906 GGAGGAGGAGGTGTGAACCCCAAGGCAGTGCCAGTGTCTCCGGCCTCAGCTTGACGCCC 965

QY 993 CCTGCGCGCGCGCGGGCGGCGACGGGGATCGGAGACGCGGCTGCAGGGCGGGGGA 1052

Db 966 CCCGCTGCAGCAGCCACAGGGCTCCCGGCTGTGGCCACCCCTACGTGGCCAGGTGCTCCT 1025

QY 1053 GGAGCGGTGCGGGGTGCCA-----AGGCGTCCGCGTGGCGCGGGCGGAGAACCG 1103

Db 1026 GGGCAGGGCGTGGGTGCTATAGTGGGCAGTGGTGGCTCGACGGCGCAGCTGACCCC 1085

QY 1104 CGAGAAAGCGCTTACGTTTCGTGTGGCGGTGATCGGAGTGTTCGTGGTGTGCTGGTT 1163

Db 1086 GGAGAAAGCGCTTACCTTCGTGTGGCTGTGGTCAATTGGCGTTCCTGCTCTGCTGGTT 1145

QY 1164 CCCCTTCTTCTTACCTACACGCTCACGGCTCACGGCCGTCCGG-----TGCTCCGTGCCACG 1214

Db 1146 CCCCTTCTTCTTACGCTACAGCCTGGCGGCCATCTGCCGGAAGCACTGCAAGGTGCCCA 1205

QY 1215 CACGCTCTTCAAAATCTTCTTCTGGTTTCGGCTACTGCAACAGCTCGTTGAACCCGGTCA 1274

Db 1206 TGGCCTCTTCCAGTTCTTCTTCTGGATCGGCTACTGCAACAGCTCACTGAACCCCTGTAT 1265

QY 1275 CTACACCATCTTCAACCAAGATTTCGCGCGCGCTTCAAGAAAGATCCTCTGTGCG 1328

Db 1266 CTACACCATCTTCAACCAAGACTTTCGCGCGTGCCTTCCGGAGGATCCTGTGCCG 1319

RESULT 2

US-09-825-923-1

; Sequence 1, Application US/09825923

; Patent No. US20010016338A1

; GENERAL INFORMATION:

; APPLICANT: Snapir, Amir

; APPLICANT: Heinonen, Paula

; APPLICANT: Alhopuro, Pia

; APPLICANT: Karvonen, Matti

; APPLICANT: Koulu, Markku

; APPLICANT: Pesonen, Ullamari

; APPLICANT: Scheinin, Mika

; APPLICANT: Salonen, Jukka T

; APPLICANT: Tuomainen, Tomi-Pekka

; APPLICANT: Lakka, Timo A

; APPLICANT: Nyyss"nen, Kristiina

; APPLICANT: Salonen, Riitta

; APPLICANT: Kauhanen, Jussi

; APPLICANT: Valkonen, Veli-Pekka

; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor

; TITLE OF INVENTION: protein, and uses thereof

; FILE REFERENCE: Alpha-2B-AR variant

; CURRENT APPLICATION NUMBER: US/09/825,923

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/422,985

; PRIOR FILING DATE: 2000-05-25

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1344

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1341)

; OTHER INFORMATION: Coding sequence for variant human

; OTHER INFORMATION: alpha-2B-adrenoceptor protein

US-09-825-923-1

Query Match 32.9%; Score 444.8; DB 10; Length 1344;

Best Local Similarity 62.4%; Pred. No. 8e-78;

Matches 820; Conservative 0; Mismatches 422; Indels 72; Gaps 5;

QY 78 CCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCTGGCCGCGCTGCTCATGCTGCT 137

Db 15 CCCCTACTCCGTGCAGGCCACAGCGCCATAGCGCGGCCCATCACCTTCCTCATCTCTT 74

QY 138 CACCGTGTTCGGCAACGTCGTCTCATCATCGCCCGTGTTCACGAGCCGCGCTCAAGGC 197

Db 75 TACCATCTTCGGCAACGCTCTGGTCTATCTCTGGCTGTGTGACGAGCCGCTCGCTGCGCGC 134

QY 198 GCGCCAAAACCTCTTCTCTGGTGTCTCTGGCCCTCGGCCGACATCCTGGTGGCCACGCTCGT 257

Db 135 CCCTCAGAACCTGTTCTCTGGTGTGCTGGCCGCGCGCATCCTGGTGGCCACGCTCAT 194

QY 258 CATCCCTTTCTCGTGGCCAAACGAGGTTCATGGGCTACTGGTACTTTCGGCAAGGCTTGGTG 317

Db 195 CATCCCTTTCTCGTGGCCAAACGAGCTGTGGGCTACTGGTACTTTCGGCGCACGTTGGTG 254

QY 318 CGAGATCTACCTGGCGCTCGACGTGCTCTTCTGACGTGCTCATCGTGCACCTGTCGCGC 377

Db 255 CGAGGTGTACCTGGCGCTCGACGTGCTCTTCTGACCTCGTCCATCGTGCACCTGTGCGC 314

QY 378 CATCAGCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTACAACTGAAGCGCAC 437

Db 315 CATCAGCCTGGACCGCTACTGGCGCGTGAGCCGCGCTGGAGTACAACTCCAAGCGCAC 374

QY 438 GCCGCGCGCATCAAGGCCCATCATCATCACCGTGTGGGTATCTCGGCCGTATCTCCTT 497

Db 375 CCCGCGCGCATCAAGTGCATCATCTCCTCATCTGTGTGGTCTATCGCCGCTCATCTCGCT 434

QY	1039	GCAGGGCCGGGGAGGAGCGCGTCGG-----GGCTGCCAAGGCGTCGCGCTGGCGCGGGCGG	1094
Db	1026	GGTGCTCTGGGCAGGGCGTGCGTCTATAGGTGGGCAGTGGTGGCGTCGACGGGGCGCA	1085
QY	1095	GCAGAACCGCGAGAAAGCGCTTCACGTTCTGTCTGGCCGTGGTTCATCGGAGTGTTCTGGGT	1154
Db	1086	GCTACCCGGGAGAACGCTTCACCTTCGTGCTGGCTGGTTCATTTGGCGTTTTTGTGCT	1145
QY	1155	GTGCTGGTTCCCTTCTTCTTCACCTACACGCTCACGGCCGTCGG-----GTGCTC	1205
Db	1146	CTGCTGGTTCCCTTCTTCTTCAGCTACAGCCTGGGCGCCATCTGCCGAAGCACTGCAA	1205
QY	1206	CGTGCCACGCACGCTCTTCAAATTCTTCTTCTGGTTCCGCTACTGCAACAGCTCGTTGAA	1265
Db	1206	GGTGCCCCATGGCCTCTTCCAGTCTTCTTCTGGATCGGCTACTGCAACAGCTCACTGAA	1265
QY	1266	CCCGGTCACTACACCATCTTCAACCCACGATTTCCGGCGCGCTTCAAGAAGATCCTCTG	1325
Db	1266	CCCTGTTATCTACACCATCTTCAACCCAGGACTTCCGGCGTGCTTCCGGAGGATCCTGTG	1325
QY	1326	TCG	1328
Db	1326	CCG	1328

RESULT 5

US-10-060-795B-10
; Sequence 10, Application US/10060795B
; Publication No. US2003004002A1
; GENERAL INFORMATION:

APPLICANT: Civelli Olivier
APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Machida, Curtis A.

; TITLE OF INVENTION: Dopamine Receptors and Genes

; FILE REFERENCE: 90-1092-CCC

; CURRENT APPLICATION NUMBER: US/10/060,795B

; CURRENT FILING DATE: 2002-01-29

;
; PRIOR APPLICATION NUMBER: 09/238977

; PRIOR FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: 08/474892

; PRIOR FILING DATE: 1995-06-07

;; PRIOR APPLICATION NUMBER: 07/973588

;; PRIOR FILING DATE: 1992-11-09

;; PRIOR APPLICATION NUMBER: 07/438544

; PRIOR FILING DATE: 1989-11-20

;; PRIOR APPLICATION NUMBER: 07/2733373

;; PRIOR FILING DATE: 1988-11-18

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 2482

TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:

; NAME/KEY: CDS

; LOCATION: (34) .. (1362)

US-10-060-795B-10

Query Match	12.8%;	Score 172.8;	DB 9;	Length 2482;
Best Local Similarity	48.9%;	Pred. No. 4.1e-25;		
Matches 595; Conservative		0; Mismatches 602;	Indels 21; Gaps 4;	

QY	115	CTGGCGGCCCTGCTCATGCTGCTCACCGTGTTTCGGCAACGTGCTCGTCATCATCGCCGTG	174
Db	151	CTGCTCACCCCTGCTCATCGCTGTCATCGTCTTCGGCAACGTGCTGGTGTGTCATGGCTGTG	210
QY	175	TTACAGAGCGCGCGCTCAAGGCGCCCAAAACCTCTTCCTGGTGTCTCTGGCCTCGGCC	234
Db	211	TCCCGCGAGAAGCGCTGCAGACCACTACCTGATCGTCAGCCTCGCAGTGGCC	270
QY	235	GACATCCTGTGGCCACGCTCGTCAATCCCTTTCTCGCTGGCCAAACGAGGTCTATGGGCTAC	294

Db 1339 GCCTTCTGAAGATCCTC 1356

RESULT 6

US-09-954-531-995

; Sequence 995, Application US/09954531

; Patent No. US20020165180A1

; GENERAL INFORMATION:

; APPLICANT: Weaver, Zoe

; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand

; FILE REFERENCE: 689290-77

; CURRENT APPLICATION NUMBER: 2002-05-02

; PRIOR APPLICATION NUMBER: US/60/233,133

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US/60/234,009

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US/60/234,034

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US/60/234,509

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: US/60/234,567

; NUMBER OF SEQ ID NOS: 1392

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 995

; LENGTH: 2625

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-954-531-995

Query Match 12.6%; Score 170.2; DB 9; Length 2625;

Best Local Similarity 48.7%; Pred. No. 1.3e-24;

Matches 593; Conservative 0; Mismatches 603; Indels 21; Gaps 4;

QY 115 CTGGCCGGCCTGCTCATGTGCTCACCGTGTTCGGCAACGTGCTCGTCATCATCGCCGTG 174

Db 283 CTGCTCACCTGCTCATCGCTGTCTGCTTTCGGCAACGTGCTGCTGTCATGGTGTG 342

QY 175 TTCACGAGCGCGCTCAAGCGGCCCAAACTCTTCCTGGTGTCTCTGGCCTCGGCC 234

Db 343 TCCCGGAGGAGCGCTGCAGACCACCACCACTACCTGATCGTCAGCCCTCGCAGTGGCC 402

QY 235 GACATCTGTTGGCCACGCTCGTCATCCCTTTCTCGTGGCCAAACGAGGTATGGGCTAC 294

Db 403 GACCTCTCGTCGCCACACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 462

QY 295 TGGTACTTCGGCAAGGCTTGGTGGGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCA 354

Db 463 TGGAAATTCAGCAGGATTCACTGTGACATCTTCGTCACCTGGACGTCAATGATGTCACG 522

QY 355 TCGTCACTCGTGACCTGTGGCCATCAGCCTGGACCGCTACTGTTCCATCATCACAGGCC 414

Db 523 GCGAGCATCTGAACCTTGTGTGCCATCAGCATCGACAGGTACACAGCTGTGGCCATGCC 582

QY 415 ATCGAGTACAACCTGAAGCGACGCGCGCGCCGATCAAGGCCGCTCATCATCACCTGTGG 474

Db 583 ATGCTGTACAATACGCGTACAGCTCAAGCGCGCGCTCATCATCATCATCATCATCATCAT 642

QY 475 GTCATCTCGGCGCTCATCTCTTCGCGCGCTCATCTCCATCGAGAAGAAGGGCGCGGCC 534

Db 643 TGGGTCCTGCTCTTCAACCATCTCTCTGCGCACTCTCTTCCGACTCAATAACGCAGACC 702

QY 535 GCGGCGCGCGAGCGCGCGCTGCGGCTGCGAGATCAACGACAGAGTGGTACGTATC 594

Db 703 AACGAGTGATCATTTGCCAACCCCGCCTTCGTGGTCTAC-----TCCTCCATC 750

QY 595 TCGTCGTGATCGGCTCTCTTCTGCTCCCTGCTCATCATCATCATCATCATCATCATCAT 654

Db 751 GTCTCCTTCTACGTGCCCTTCTTGTACCCCTGCTGCTTCTACATCAAGATCTACATTGC 810

QY 655 ATCTACCAGATCGCAAGCGTTCGCACCCCGGTGCCACCCAGCGCGGGGTCCGGACGCC 714

Db 811 CTCCGACAGCCGCAAGCGAGTCAACACCAACGCGAGCCGAGCTTTCAGGGCCAC 870

QY 715 GTCGCCGCGCGCGCGGGGGACCGAGCGCAGGCCCAACGGTCTTGGGCCCCGAGCGCAGC 774

Db 871 CTGAGGGCTCCACTAAAGGGCACTGTACTCACCCCGAGGACATGAAACTCTGCACCGTT 930

QY 775 GCGGGCCCGGGGGCGCAGAGCGCAACCGTGTGCCACCCAGCTCAACGGCGCCCTTGGC 834

Db 931 ATCATGAAGTCTAATGGGAGTTTCCAGTGAACAGGGGAGAGTGGAGGCTGCCCGCGCA 990

QY 835 GAGCCCGCGCGCGCGCGCGCGGACACCGACCGCTGGAGCTGGAGGAGAGTCTGCT 894

Db 991 GCCCAGGAGCTGGAGATGAGATGCTCTCCAGCACCAAGCCAGCCCGAGAGACCCGGTAC 1050

QY 895 TCCGACCAACCGCGAGCGGCTTCCAGGGCCCCCGCAGACCCGAGCGGTTCCCGGGGCAAA 954

Db 1051 AGCCCCATCCACCCAGCCACCACCGTACTCTCCCCGACCGTCCACACCGTCTC 1110

QY 955 GGCAAGGCCGAGCGAGCGAGGTGAAGCCGGCGACA----GCCTGCCGCGCGCGGCC 1010

Db 1111 CACAGCACTCTGACAGCCCCCGCAACAGAGAAATGGGATGCCAAAGACCAACCCC 1170

QY 1011 GGGGGCGACGGGATCGGACCGCGGCTGCAGGGCGGGGAGGAGCGCGTCCGGGGTGC 1070

Db 1171 AAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGACCTCCCTC 1230

QY 1071 CAAGGC--GTCGCGCTGGCGCGGGGCGGAGAACCGCGAGAACGGCTTCACGTTCTGCTG 1128

Db 1231 AAGACCATGAGCCGTAGAAAGCTCTCCAGCAGAGGAGAAAGAACCCACTCAGATGCTC 1290

QY 1129 GCGGTGTCATCGGAGTGTTCGTGGTGTGCTGGTTCCTTCTTTCACCTACACGCT- 1187

Db 1291 GCCATTGTTCTCGGCGTGTTCATCATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1350

QY 1188 --CACGGCCGTGCGGTGCTCCGTGCCACGACGCTCTTCAAATTCCTTCTTCTGTTCCGC 1245

Db 1351 AACATACACTGTGACTGCAACATCCCGCTGTCTGTACAGCGCTTACAGTGGCTGGGC 1410

QY 1246 TACTGCAACAGCTCGTTGAACCCGGTTCATCTACACCATCTTCAACCAAGATTTCCGCCGC 1305

Db 1411 TATGTCAACAGCGCGCTGAACCCCATCATCTACACCACTTCAACATTGAGTTCCGCAAG 1470

QY 1306 GCCTTCAAGAAAGATCCT 1322

Db 1471 GCCTTCTGAAGATCCT 1487

RESULT 7

US-09-349-755-3

; Sequence 3, Application US/09349755

; Patent No. US20020166131A1

; GENERAL INFORMATION:

; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman

; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/349,755

; FILING DATE: 08-Jul-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/09/042,780
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-349-755-3

Query Match      12.4%; Score 168; DB 9; Length 1335;
Best Local Similarity 51.4%; Pred. No. 3.2e-24;
Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAGCCGGACGCGGCGCAACCGAGCTGGAACGGGACCGAGGCGCGGGGG 62
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Db 6 GCGCGCGCGCGCGCGCGCTTCTCGGAGCGCTTCGGGCGCGCTGGCGGCGGCGCGGC 65
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QY 63 CGGCGCCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCTGGCCGG 122
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Db 66 GCGGCGCGGGCGCGCGCTTCTCGGCAGCCTGGACCGCGGTGCTGGCCGCGCTCATGGC 125
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QY 123 CTGCTCATGTGCTCACCGTGTTCGGCAACGTGCTCGTCATCATCGCCGTTTCACGAG 182
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Db 186 CTCGAGCCTCCGCACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCT 245
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QY 243 GGTGGCCACGCTCGTATCCCTTTCTCGCTGGCCAAAGAGGTGATGGCTACTGTTACTT 302
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QY 303 CGGCAAGGCTTGGTGGAGATCTACCTGGCGCTGACAGTGTCTTCTGACAGCTGTCAT 362
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Db 306 CGGCCGGGCTCTGCAAGCTGTGGCTGTGTGGACTACCTGCTGTGACCTCTCTTGC 365
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QY 363 CGTGACCTGTGCGGCATCAGCCTGGACCGCTACTGTTCCATCACACAGGCCATCGAGTA 422
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Db 366 CTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCGTCAACCGAGGCTCTATA 425
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QY 423 C---AACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCACCCTGTGGTTCAT 479
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Db 426 CCGGCGCCAGCAGGCTGACACGCGCGGCGAGTGCAGAGATGCTGTGTGGTGTGCT 485
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QY 480 CTCGGCGGTATCTCTTCCCGCGCTCATCTCCATCGAAGAGGCGCGCGCGCGG 539
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Db 486 GGCCTTCTCTGTGTCGACCAAGCCATCTGAGCTGGAGTACCTGTCCGGGGCAGCTC 545
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QY 540 CCCGCGCGCGCGCGCTGGAGATCAACGACCAAGTGGTACGTATCTCTGTC 599
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Db 546 CATCCCCGAGGGCCACTGCTATGCCGAGTTCTTACAACTGGTACTTCTCATACGCGC 605
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QY 600 GTGCATCGGCTCTTCTTCTGCTCCCTCATCATGATCCTGTTACGTGCGCATCTA 659
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Db 606 TTCCACCTTGAGTTCTTTACGCGCTTCTCAGCGTCACTTCTTTAACCTCAGCATCTA 665
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 660 CCAGATCGCAAGCGTGCACCCGCGTGCACCCAGCCGCGCGGCGTCCGGACGCGCTCGC 719
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Db 666 CCTGAACATCCAGAGGCGCACCCGCTCCGGCTGGATGGGCTCGAGAGGCGCGGCC 725
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QY 720 CGCGCCCGCGGGGCGCACCGAGCGCAGGCCCAACGGTCTG---GGCCCCGAGCGCGC 776
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Db 726 CGAGCCCCCTCCCGAGGCGCCAGCCCTCACCACCCACCGCCTGGTGTGGGGTGTG 785
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QY 777 GGGCCCGGGGGCGCAGAGGCGGCAACCGCTGCCCCACCCAGCTCAACGGCGCCCCCTGGCGA 836
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 786 GCAGAGGGGCGACGGGAGGCCATGCCGCTGCACAGGTATGGGTGGGTGAGGCGCGCT 845
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QY 837 GCGCGCGCGCGCGCGG 852
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Db 846 AGCGCTGAGGCGCGG 861
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RESULT 8
US-09-166-334-3
; Sequence 3, Application US/09166334
; Patent No. US20020168708A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-166-334-3
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Query Match      12.4%; Score 168; DB 9; Length 1335;
Best Local Similarity 51.4%; Pred. No. 3.2e-24;
Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAGCGGACGCGGCAACCGAGCTGGAACGGGACCGAGGCGCGGGGG 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 GCGCGCGCGCGCGCGCGCTTCTCGGAGCGCTTCGGGCGCGTGGCGGCGGCGCGC 65
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 CGGCGCGCGCGCGCGCGCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCTGGCCGG 122
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Db 66 GGCGGGCGGGCGCGGCTTCTCGGCAGCCTGGACCGGCTGGCGGCTCATGGC 125
QY 123 CCTGCTCATGCTGCTCACCGTGTTCGGCAACGTCGTCGTCATCATCGCCGTTTCACGAG 182
Db 126 GCTGCTCATGTCGGCCACGGTGTGGCAACGCGTGGTCATGCTGCCTTCGTGGCGCA 185
QY 183 CCGCGCGCTCAAGGCGCGCCCCAAACCTTCTCCTGGTGTCTCTGGCCTCGGCCGACATCCT 242
Db 186 CTCGAGCCTCCGACCCAGAACACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCCT 245
QY 243 GGTGGCCACGTCGTCATCCCTTTCTCGCTGGCCAAACGAGGTATGGGCTACTGGTACTT 302
Db 246 CGTCGGCGCCTTCTGCATCCCACTGTATGTACCCTACGTGCTGACAGGCCGCTGGACCTT 305
QY 303 CGGCAAGGCTTGTGTCGAGATCTACCTGGCGCTCGACGTGCTTCTGACGTCGTCCAT 362
Db 306 CGCGCGGGCCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACCTCCTCTGC 365
QY 363 CGTGACCTGTGCGGCATCAGCCTGGACCGTACTGGTCCATCAACAGGCCATCGAGTA 422
Db 366 CTTCAACATCGTGTCTCATCAGTACGCTACGACCGGCTTCTGTGCGTACCGAGCGGTCTCATA 425
QY 423 C---AACCTGAAGCGCACGCGCGCGCATCAACAGGCCATCATCATACCCGTGTGGTCA 479
Db 426 CCGGCGCCACGAGGTGACACGCGCGGCGAGTGCAGGAGATGCTGTGGTGTGGTGTCT 485
QY 480 CTCGGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGCGCGCGCGG 539
Db 486 GGCCTTCTGCTACGACACGACCATCTCTGAGTGGGAGTACCTGTCCGGGGCAGCTC 545
QY 540 CCGCAGCGCGCGCGGCTCGGAGATCAACGACCAAGAGTGGTAGCTCATCTCGTC 599
Db 546 CATCCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACCTGGTACTTCTCTCATCACGGC 605
QY 600 GTGCATCGGCTCCTTCTTCTGCTCCCTGCTCATCATGATCCTGGTCTACGTGCGCATCTA 659
Db 606 TTCCACCTTGAGTTCTTTACGCCCTTCTCTCAGCGTACCTTCTTTAACCTCAGCATCTA 665
QY 660 CCAGATGCGCAAGCTCGACCCGCGTGCCACCCAGCGCGGGGTCCGGACGCGCTCGC 719
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QY 720 CGCGCGCGCGGGGCAACCGAGCGAGGCGCCAAACGGTCTG---GGCCCCGAGCGCAGCGC 776
Db 726 CGAGCCCGCTCCCGAGGCGCCAGCCCTCACCAACCCCGCCCTGGCTGCTGGGCTGCTG 785
QY 777 GGGCGCGGGGCGCAGAGGCGGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGA 836
Db 786 GCAGAAAGGGCACGGGAGGCGCATGCCGCTGCACAGGTATGGGGTGGGTGAGGCGCGCT 845
QY 837 GCGCGCGCGCGCGCGG 852
Db 846 AGCGGCTAGGCGCGG 861

RESULT 9
US-09-350-206-3
; Sequence 3, Application US/09350206
; Patent No. US2002099199A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,206
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-350-206-3

Query Match 12.4%; Score 168; DB 10; Length 1335;
Best Local Similarity 51.4%; Pred. No. 3.2e-24;
Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;
QY 3 GGGCTCCCTGCAGCCGACGCGGGCAACGCGAGCTGGAACGGACCGAGCGCGCGGGG 62
Db 6 GCGCGCGCGCGCGCGCTGAACGCTTCGGGGCGGCTGGCGGCGAGCGCGCGG 65
QY 63 CGGCGCGCGCGCGCGCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCTGGCGG 122
Db 66 GCGCGCGCGCGCGCGCTTCTCGGCAGCCTGGACCGGCTGCTGGCGCGGCTCATGGC 125
QY 123 CTTGCTCATGCTGCTCACCGTGTTCGGCAACGTCGTCGTCATCATCGCCGTTTCACGAG 182
Db 126 GCTGCTCATGCTGGCCACGTCGTCGGCAACGCGCTGGTTCATGCTCGCCTCGTGGCGCA 185
QY 183 CCGCGCGCTCAAGGCGCGCCAAACCTCTTCTGCTGGTGTCTCTGGCCTCGGCCGACATCCT 242
Db 186 CTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCCT 245
QY 243 GGTGGCCACGCTCGTCATCCCTTTCTCGCTGGCCAAACGAGGTATGGGCTACTGGTACTT 302
Db 246 CGTCGGCGCCTTCTGCATCCCACTGTATGTACCTACGTCGTGACAGGCCGCTGACCTT 305
QY 303 CGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTCGCTCTTCTGACGTCGTCAT 362
Db 306 CGCGCGGGCCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACTCTCTCTGC 365
QY 363 CGTGCACTGTGCGCCATCAGCCTGGACCGCTACTGTGTCATCAACAGGCCATCGAGTA 422
Db 366 CTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTCTGTCGCTACCCGAGCGGTCTCATA 425
QY 423 C---AACCTGAAGCGCACGCGCGCGCATCAAGGCCATCAACGTCATCATCACCGTGTGGTCA 479
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QY 480 CTCGGCGCTCATCTCCTTCCCGCGCTCATCTCCATCGAGAGAAGGCGCGCGCGG 539
Db 486 GGCCTTCTGCTGACGACCGCATCTGAGTGGGAGTACCTGCTCCGGGGCAGCTC 545
QY 540 CCGCAGCGCGCGCGCGCTGCGGAGTCAACGACCAAGTGGTAGCTCATCTCGTC 599
Db 546 CATCCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACCTGGTACTTCTCTCATCACGGC 605

QY 600 GTGCATCGGCTCCTTCTCGCTCCCTCATGATCCTGGTCTACGTGGCGCATCTA 659
Db 606 TTCCACCCCTGAGTCTTTACGCCCTTCTCAGCGTCACTTTCTTAACCTCAGCATCTA 665
QY 660 CCAGATCGCCAAAGCGTCCGACCCGCGTCCACCCAGCCCGCGGGTCCGGACCCGTCGC 719
Db 666 CCTGAACATCCAGAGCGCACCCGCTCCGGCTGGATGGGGTCGAGAGGCAGCCGGCC 725
QY 720 CGCGCCCGCGGGGCGACCGAGCGGAGGCCCAACGGTCTG---GGCCCCGAGCGCAGCGC 776
Db 726 CGAGCCCCCTCCGAGGCCAGCCCTCACACCCACCCGCTGGCTGTGGGGTCTGTG 785
QY 777 GGGCCCGGGGGCGCAGAGCGGAGCGGAGCCAGCTGCCACCCAGCTCAACGGCCCTGGCGA 836
Db 786 GCAGAGGGGCGACGGGAGGCCATGCGGCTGCACAGGTATGGGGTGGGTGAGGCGCGCT 845
QY 837 GCGCGCGCGCGCGG 852
Db 846 AGCGCTGAGGCGCGG 861

RESULT 10

US-09-349-755-1
; Sequence 1, Application US/09349755
; Patent No. US20020166131A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; ..
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,755
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-349-755-1

Query Match 12.4%; Score 168; DB 9; Length 2689;
Best Local Similarity 51.4%; Pred. No. 3.5e-24;
Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGACCCGACCGCGGCAACGCGAGCTGGAACGGAGCGCGCGGGG 62
Db 296 GCGCGCGCGCGCGACGGCGCGTGAACGCTTGGGGGCGCTGGCGGCGAGCGCGGC 355
QY 63 CGCGCCCGCGGCGCACCTTACTTCCCTGACAGGTGACGCTGAGCTGGTGTGCTGGCGG 122
Db 356 GCGGGGCGGCGCGGCTTCTCGGAGCCTGGACCGGCTGCTGGCGCGCTCATGGC 415
QY 123 CCTGCTCATGCTGCTACCGTGTTCGCAACGCTGCTGCTCATCATCGCCGTGTTTACGAG 182
Db 416 GCTGCTCATGCTGCGCACGGTGTGCGCAACGCGCTGGTGTGCTGCTGCGCTTCTGCGCGA 475
QY 183 CGCGCGCTCAAGGCGCCCCAACTTCTTCTGGTGTCTCTGGCTCGGCGCGACATCCT 242
Db 476 CTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCATCTCCGACTTCT 535
QY 243 GGTGGCCACGCTGCTCATCCCTTCTCGCTGGCCAAAGAGTCTATGGGCTACTGGTACTT 302
Db 536 CGTCGGCGCTTCTGCATCCCACTGTATGTACCTACGTGTGACAGGCGCTGGACCTT 595
QY 303 CGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGCTTCTGACGCTGCTCAT 362
Db 596 CGGCCGCGCTTCTGCAAGCTGTGGTGGTAGTGGACTACCTGCTGTGACCTCCTCTGC 655
QY 363 CGTGACCTGTGCGCCATCAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
Db 656 CTTCAACATGCTGCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715
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Db 776 GGCCTTCTGCTGTACGACCGACCATCTGAGCTGGAGTACCTGTCCGGGGGAGCTC 835
QY 540 CCGCAGCGCGCGCGCGCGCTGCGAGATCAACGACGAGAGTGGTACGTATCTCTGCTC 599
Db 836 CATCCCGAGGGCCACTGCTATGCGGAGTTCTTCTAACAACTGGTACTTCTCTCATCACGGC 895
QY 600 GTGCATCGGCTCCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
Db 896 TTCCACCTGGAGTTCTTACGCCCTTCTCAGCGTCACTTCTTAACTCAGCATCTA 955
QY 660 CCAGATCGCCAAAGCGTCCGACCCGCGTCCACCCAGCGCGCGCGCGCGCGCGCGCGC 719
Db 956 CCTGAACATCCAGAGCGCACCGCGCTCCGCGTGGAGTGGGCTCGAGAGGCGCGCGCGC 1015
QY 720 CGCGCCCGCGGGGCGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 776
Db 1016 CGAGCCCCCTCCCGAGGC 1075
QY 777 GGGCCCGGGGGCGCAGAGC 836
Db 1076 GCAGAAGGGGCGACGGGAGGCCATGCGGCTGCACAGGTATGGGGTGGGTGAGGCGCGCGT 1135
QY 837 GCGCGCGCGCGCGCGG 852
Db 1136 AGCGCTGAGGCGCGG 1151

RESULT 11
US-09-166-334-1
; Sequence 1, Application US/09166334
; Patent No. US20020168708A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street

QY 378 CATCAGCCTGGACCGCTACTGGTCCCATCACACAGGCCATCGAGTACAACTGAAGCGCAC 437
|||||
Db 744 CATCTCCGTGGACCGGTACGTGGCGGTGCGCCACTCACTCAAGTACCCAGCCATCATGAC 803

QY 438 GCCGCGCGCATCAAGGCCATCATCATACCGGTGTGGGTGATCTCGGCCGTCTATCTCTT 497
|||||
Db 804 CGAGCGCAAGGCGCGCCATCCTGGCCCTGCTCTGGTCTGAGTGGTGTGCTCGT 863

QY 498 CCCGCGCGTCACTCCATCGAGAAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 557
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Db 864 AGGCCCCCT-----GCTGGGCTGGAAGAGAGCGCGCGCGCGCGCGCGCGCGCG 908

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Db 909 CTTCTGCGGTATACCGAGGAGCGGCTACGCTGTCTTCTCTCGGTGTGCTCCTTCTA 968

QY 618 CGCTCCCTGCCTCATCATGATCCTGGTCTACGTGCGCATCTACCATGATCGC-----CAA 671
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Db 969 CTTGCCCCATGGCGGTATCGTGGTATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1028

QY 672 GCGTCGACCGCGTCCACCCAGCGCGCGGGTCCGACGCCGTCCCGCGCGCGCGCGCG 731
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Db 1029 CACGCGACGCTCGAGCAGGCGCTCAAGCGCGAGGAGGCAAGGCTCCGAGGTGGTCT 1088

QY 732 GGGCACCAGCGAGGCCCAACGGTCTGGGCCCCGAGCGCAGCGCGCGCGCGCGCGCG 791
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Db 1089 GCGCATCCACTGTGCGGCGCGGCCACGCGGCGCGCGCGCGCGCGCGCGCGCGCG 1148

QY 792 AGAGGCCGAACCGCTGCCACCCAGCTCAACGGCGCGCGCGCGCGCGCGCGCGCG 844
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Db 1149 CAAGGCCACACCTTCCGACGCTCGCTCTCCGTGCGCGCTGCTCAAGTCTTCCC 1201

RESULT 14
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; Sequence 1, Application US/10005010
; Patent No. US20020115149A1
; GENERAL INFORMATION:
; APPLICANT: Weinshank et al, Richard L.
; TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
; TITLE OF INVENTION: Selective Compound
; FILE REFERENCE: 36536-BA
; CURRENT APPLICATION NUMBER: US/10/005,010
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(1414)
US-10-005-010-1

Query Match 10.9%; Score 147.2; DB 12; Length 1645;
Best Local Similarity 52.9%; Pred. No. 3.5e-20;
Matches 348; Conservative 0; Mismatches 298; Indels 12; Gaps 1;

QY 67 GCCCGGCGCACCCCTTACTCCCTGCGAGGTGACGCTGAGCTGGTGTGCTGCGCGCGCCTG 126
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Db 365 GCTTGGATCCAGGACCCCTCCAGGCGCTCAAGATCTCCCTGCGGTGGTCTTCCGTC 424

QY 127 CTCATGCTGCTACCGTGTTCGGAACGTGCTGTCATCATCGCGCTGTTTACGAGCCGC 186
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Db 425 ATCACACTGGCCACAGTCTCTCCATGCTTGTACTCACCATCTTACTCACCAGG 484

QY 187 GCGCTCAAGGCGCCCCAAACCTTCTCTGGTGTCTGTGCGCTGCGCGCGACATCTGGTG 246
|||||
Db 485 AAGCTCCACACCCCTGCCAACTACCTGATGGCTCCCTGGCCACCGACCTCTTGTT 544

QY 247 GCCACGCTCGTCACTCCCTTTCTCGCTGGCCAAAGAGGTATGGGCTACTGGTACTTCGC 306
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Db 545 TCCATCTTGGTAATGCCCATCAGCATCGCCTATACCATCACCCACACCTTGGACCTTGGC 604

QY 307 AAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGCTCTTCTGACGTCGTCTCATCGTG 366
|||||
Db 605 CAAATCTTGTGACATCTGGCTGTCTCTGACATCAGTGTGACAGCTTCCATCTCATCTG 664

QY 367 CACCTGTGCGCCATCAGCCTGGACCGCTACTGGTCCATCACAGGCCCATCGAGTACAC 426
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Db 665 CATCTCTGTGTCATCTCTGGACAGTACTGGCAATCACAGATGCTTGGGCCATCTCCATC 724

QY 427 CTGAAGCGCACGCGCGCGCATCAAGGCCCATCATCATCACCGTGTGGTCTATCTCGGCC 486
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QY 487 GTCATCTCCTTCCCGCGCTCATCTCCATCGAGAAAGGCGCGCGCGCGCGCGCGCGCAG 546
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QY 607 GGCTCCTTCTTCCCTCCCTGCCTCATCATGATCTGCTGTCAGTGGCGCATCTACCATC 666
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Db 953 GCCCGGAACCGCATCTCTGAATCCACCTCACTCTATGGGAAGCGCTTACACACGCGCC 1010

RESULT 15
US-09-864-761-3769/c
; Sequence 3769, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3769
; LENGTH: 1973
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049576.15
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
US-09-864-761-3769

Query Match      10.9%; Score 147.2; DB 10; Length 1973;
Best Local Similarity 52.9%; Pred. No. 3.6e-20;
Matches 348; Conservative 0; Mismatches 298; Indels 12; Gaps 1;

QY 67 GCCCGGGCCACCCCTTACTCCCTGACGGTGACGCTGGTGTGCCTGGCGGGCCTG 126
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Db 1234 GCTTGGGATCCCAGGACCCTCCAGGCGCTCAAGATCTCCCTTGCCGTGGTCCTTCCGTC 1175

QY 127 CTCATGCTGCTCACC GTGTTGCGGCAACGTGCTCGTCATCATCGCCGTGTTACAGAGCCGC 186
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Db 1174 ATCACACTGGCCACAGTCTCTCCAATGCCTTGTGTA CTACCA CCACTCTTACTCACCAGG 1115

QY 187 GCGCTCAAGGCGCCCAAAACCTCTTCCCTGGTGTCTTGGCCTCGGCCGACATCCTGGTG 246
   |||||
Db 1114 AAGCTCCACACCCCTGCCAACTACCTGATTGGCTCCCTGGCCACCACCGACCTCTTGGTT 1055

QY 247 GCCACGCTCGTCATCCCTTTCTCGTGGCCCAACGAGGTCA TGGGCTACTGGTACTTCGGC 306
   |||||
Db 1054 TCCATCTTGGTAATGCCCATCAGCATCGCCTATACCATCACCCACACCTGGAACCTTTGGC 995

QY 307 AAGGCTTGGTGGGAGATCTACCTGGCGCTCGACGTGCTCTTCTGACGTCGTCCATCGTG 366
   |||||
Db 994 CAAATCTTGTGTGACATCTGGCTGTCTCTGACATCACGTGTGCACAGCCTCCATCCTG 935

QY 367 CACCTGTGGCCCATCAGCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTACAAC 426
   |||||
Db 934 CATCTCTGTGTCA TGTCTGTGACAGGTACTGGGCAATCACAGATGCCCTGGAATACAGT 875

QY 427 CTGAAGCGCACGCGCGCCGCATCAAGGCCATCATCACCGTGTGGGTCACTCGGCC 486
   |||||
Db 874 AAACGCGAGGACGGCTGGCCACGCGCCACCATGATGCCATTGTCTGGGCCATCTCCATC 815

QY 487 GTCATCTCCTTCCCGCCGCTCATCTCCATCGAGAAGAAGGGCGGCGGCGGCGGCCGAG 546
   |||||
Db 814 TGCATCTCCATCCCCCGCTCTTCTGGCGCAGGCCAAGGC-----CCAGGAG 767

QY 547 CCGGCGGAGCGCGCTGCGAGATCAACGACCAGAGTGGTACGTCTATCTCGTGCATC 606
   |||||
Db 766 GAGATGTCGGACTGTCTGGTGAACACCTCTCAGATCTCTACACCATCTACTCCACTGT 707

QY 607 GGCTCCTTCTTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGCGCATCTACCAATC 666
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Db 706 GGGGCCCTTCTACATTCCTCGGTGTTGCTCATCATCTATATGCGCGGATCTACCGGGCT 647

QY 667 GCCAAGCGTCGACCCGCGTGCCACCCAGCCGCGGGTCCGGAGCCCGTCCGCCGCGC 724
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Db 646 GCCCGGAACCGCATCCTGAATCCACCCTCACTCTATGGGAAGCGCTTCACCACGCGCC 589
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:24:01 ; Search time 1612.04 Seconds
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1350	100.0	1350	23	AAI99917 Human alpha-2AAR e
2	1348.4	99.9	1350	23	AAI99918 Human alpha-2AAR v
C 3	917	67.9	1733	24	ABQ47500 Oligonucleotide fo
4	917	67.9	1733	24	ABQ47501 Oligonucleotide fo
C 5	917	67.9	7353	24	ABL32073 Human immune syste
C 6	917	67.9	7353	24	AAD28363 Human chemically t
7	838	62.1	1733	24	ABQ47498 Oligonucleotide fo
C 8	838	62.1	1733	24	ABQ47499 Oligonucleotide fo
9	838	62.1	7353	24	ABL32072 Human immune syste

10	838	62.1	7353	24	AAD28362 Human chemically t
11	530.6	39.3	1383	23	AAI99931 Human alpha-2CAR e
12	517.6	38.3	1371	23	AAI99933 Human alpha-2CAR v
13	514	38.1	1382	15	AAQ64890 Human derived adre
14	444.8	32.9	1344	22	AAD04761 Human alpha2B-adre
15	444.4	32.9	1344	23	AAI99906 Human alpha-2BAR t
16	443	32.8	1353	22	AAD04762 Human alpha2B-adre
17	441.4	32.7	1353	23	AAI99905 Human alpha-2BAR t
18	422.2	31.3	2064	12	AAQ14151 Human alpha 2 beta
19	422.2	31.3	2064	18	AAT59499 Human alpha-2b adr
C 20	328.8	24.4	4850	24	AAD28395 Human chemically t
21	260.6	19.3	1431	18	AAT85635 Balanus amphitrite
C 22	258.2	19.1	6904	24	ABL32075 Human immune syste
C 23	258.2	19.1	6904	24	AAD28365 Human chemically t
24	230.2	17.1	4850	24	AAD28394 Human chemically t
25	223.4	16.5	1140	18	AAT88392 Corn barnacle G-pr
26	200.4	14.8	1845	21	AAZ98400 Canine betal-adren
27	200.4	14.8	1845	21	ABK40732 Dog betal-adrenoce
28	189	14.0	4401	21	AAZ98404 Rhesus monkey beta
29	189	14.0	4401	24	ABK40736 Monkey betal-adren
30	188.6	14.0	1637	22	AAF61182 Human betal-adreno
31	188.6	14.0	1637	22	AAF61183 Human betal-adreno
32	188.6	14.0	1637	22	AAF61184 Human betal-adreno
33	188.6	14.0	1637	22	AAF61185 Human betal-adreno
34	188.6	14.0	1637	22	AAF61186 Human betal-adreno
35	188.6	14.0	1637	22	AAF61187 Human betal-adreno
36	188.6	14.0	1637	22	AAF61188 Human betal-adreno
37	188.6	14.0	1637	22	AAF61189 Human betal-adreno
38	188.6	14.0	1723	21	AAA38338 Human beta-adrener
39	188.6	14.0	1723	21	AAZ98399 Human betal-adreno
40	188.6	14.0	1723	24	ABK92208 Prostate cancer-as
41	188.6	14.0	1723	24	ABK40731 Human betal-adreno
42	178.2	13.2	1525	21	AAZ98405 Mouse betal-adreno
43	178.2	13.2	1525	24	ABK40737 Mouse betal-adreno
44	177.4	13.1	44242	23	ABL19930 Drosophila melanog
45	177	13.1	1038	23	ABL19931 Drosophila melanog

ALIGNMENTS

RESULT 1
AAI99917
ID AAI99917 standard; DNA; 1350 BP.
XX
AC AAI99917;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2AAR encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase;
KW phosphorylation; inositol phosphate; alpha-2AAR;
KW GenBank Accession AF281308; chromosome 10; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /*tag= a
FT /product= "alpha-2AAR"
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.

XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52122.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Example 7; Page 151; 163pp; English.
PS
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (GenBank Accession AF281308).
XX
SQ Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;

Query Match 100.0%; Score 1350; DB 23; Length 1350;
Best Local Similarity 100.0%; Pred. No. 1.4e-203;
Matches 1350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTCCCTGCAGCCGGACGGGGCAACCGGAGCTGGACGGGACCGAGGCGCGGGG 60
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QY 61 GGCGGCGCGCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGCCTGGCC 120
Db |||||
QY 121 GGCCCTGCTCATGCTGCTCACCCTGTTTCGGCAACCGTGTCTGCTGCTGCTGCTGCTG 180
Db |||||
QY 181 AGCCGCGCGCTCAAGGCGCCCCAAACCTTCTCTGGTGTCTGCTGGCCCTCGGCCGACATC 240
Db |||||
QY 241 CTGGTGGCCACGCTCGTCATCCCTTTCTCGCTGGCCAAACGAGGTGCTGGGCTACTGGTAC 300
Db |||||
QY 301 TTCGGCAAGGCTTGGTGGGAGATCTACCTGGCGCTCGACGTGCTTCTGACGTCGTCC 360
Db |||||
QY 361 ATCGTGACCTGTGGCCCATCAGCCTGGACCGCTACTGGTCCCATCACACAGGCCATCGAG 420
Db |||||

QY	421	TACAACTGAAGCGCAGCGCGCGCCGCATCAAGGCCATCATCATCACCCTGTGGTCAATC	480
Db	421		
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Db	481		
QY	541	CCGAGCCGGCGGAGCGCGCTGCGAGATCAACGACCAAGTGGTACGTCACTCTCGTCG	600
Db	541		
QY	601	TGCATCGGCTCCTTCTTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGCGCATCTAC	660
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QY	661	CAGATCGCCAAAGCGTCGACCCCGGTGCCACCGCGCGCGGTCCGGACGCCGTGCGC	720
Db	661		
QY	721	GCGCCCGGGGGCACCGAGCGCAGGCCCAACGGTCTTGGCCCCGAGCGCAGCGCGGC	780
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QY	781	CCGGGGGGCGCAGAGGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGCCC	840
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QY	841	GGCCCGCGCGGGCGCGGACACCGCGCTGACCTGGAGGAGCTCGTCTTCCGAC	900
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QY	901	CACGCGAGCGGCTCCAGGGCCCCGACACCGCGCGCGGTCCCCGGGGGAAAGGCAAG	960
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QY	961	GCCCGAGCGAGCGAGGTGAAGCGGGCGCAGCCCTGCGCGCGCGCGCGCGCGCGGACG	1020
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QY	1021	GGGATCGGGACGCCGGCTGCAGGGCGCGGGGAGGAGCGCGTCCGAGCGCTCG	1080
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QY	1081	CGCTGGCGGGCGGCGAGAACCGCGAGAACGCTTACGTTCTGCTGGCCGTGGTCAATC	1140
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QY	1141	GGAGTGTCTGGTGTGCTGGTTCCTTCTTCTTACCTACACGCTCACGGCCGTCGGG	1200
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QY	1261	TTGAACCCGGTCACTACACCATCTTCAACCCAGATTTCCCGCGCCCTTCAAGAAGATC	1320
Db	1261		
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Db	1321		

RESULT 2
AAI99918
ID AAI99918 standard; DNA; 1350 BP.
XX
AC AAI99918;
XX
DT 18-FEB-2002 (first entry)

XX Human alpha-2AAR variant encoding DNA.

DE

XX

KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;

KW polymorphic site; allelic variant; cardiovascular disease;

KW central nervous system disease; adenylyl cyclase; MAP kinase activity;

KW phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.

XX

OS Homo sapiens.

XX

FH Key

FT CDS

FT 1..1353

FT /*tag= a

FT /product= "alpha-2AAR"

FT replace(753,C)

FT /*tag= b

XX

PN WO200179561-A2.

XX

PD 25-OCT-2001.

XX

PF 17-APR-2001; 2001WO-US12575.

XX

PR 17-APR-2000; 2000US-0551744.

PR 10-AUG-2000; 2000US-0636259.

PR 19-OCT-2000; 2000US-0692077.

XX

PA (LIGGETT) LIGGETT S B.

PA (SMAL/) SMALL K M.

XX

PI Liggett SB, Small KM;

XX

DR WPI; 2001-611728/70.

DR P-PSDB; AAM52123.

XX

PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for

PT determining whether an individual is at increased risk of developing a

PT disease associated with the corresponding receptor comprises detecting

PT a polymorphic site -

XX

PS Disclosure; Page 152; 163pp; English.

XX

CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic

CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;

CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,

CC alpha2A or alpha2C or fragment or complement of; and

CC (b) detecting a polymorphic site comprising nucleotide positions 901-909

CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV

CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at

CC positions 961-972 of (III). The method may be used for genotyping an

CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine

CC whether an individual is at increased risk of developing a disease

CC associated with alpha2B, alpha2A or alpha2, comprising detecting a

CC polymorphic site which correlate to disease selected from cardiovascular

CC disease, central nervous system disease and combinations of these. In

CC addition, the technique may be used to predict an individual's response

CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,

CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and

CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,

CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of

CC these) by detecting the polymorphic site and correlating the site to a

CC predetermined response (where the response is correlated to adenylyl

CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate

CC levels). The present sequence is that of the human alpha-2AAR variant

CC gene.

XX

SQ Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;

Query Match 99.9%; Score 1348.4; DB 23; Length 1350;

Best Local Similarity 99.9%; Pred. No. 2.6e-203;

Matches 1349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTCCCTGCAGCCGGACGCGGGCAACGCGAGCTGGAACGGGACCGAGGCGCCGGGG 60

Db 1 ATGGGCTCCCTGCAGCCGGACGCGGGGAACGGAGCTGGAACGGGACCGAGGCGCGGGG 60

QY 61 GGCGGCGCGCGGGCCACCCCTTACTCCCTGCAGGTACGGTGACGGTGGTGTGCCTGGCC 120

Db 61 GGCGGCGCGCGGGCCACCCCTTACTCCCTGCAGGTACGGTGACGGTGGTGTGCCTGGCC 120

QY 121 GGCCTGCTCATGCTGCTCACCGTGTTCGGCAACGTGCTCGTCAATCATCGCCCGTGTTCACG 180

Db 121 GGCCTGCTCATGCTGCTCACCGTGTTCGGCAACGTGCTCGTCAATCATCGCCCGTGTTCACG 180

QY 181 AGCCGCGCGCTCAAGGCGCGCCCAAAACCTTCTCTGGTGTCTCTGGCCTCGGCCGACATC 240

Db 181 AGCCGCGCGCTCAAGGCGCGCCCAAAACCTTCTCTGGTGTCTCTGGCCTCGGCCGACATC 240

QY 241 CTGGTGGCCACGCTCGTCAATCCCTTTCTCGCTGGCCAAACGAGGTCAATGGGTACTGGTAC 300

Db 241 CTGGTGGCCACGCTCGTCAATCCCTTTCTCGCTGGCCAAACGAGGTCAATGGGTACTGGTAC 300

QY 301 TTCGGCAAGGCTTGGTGGAGATCTACTTGGCGGCTCGACGTGCTCTTTCACACGTCTGCC 360

Db 301 TTCGGCAAGGCTTGGTGGAGATCTACTTGGCGGCTCGACGTGCTCTTTCACACGTCTGCC 360

QY 361 ATCGTGACCTGTGCGGCCATCAGCCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAG 420

Db 361 ATCGTGACCTGTGCGGCCATCAGCCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAG 420

QY 421 TACAACCTGAAGCGCACGCCGCGCATCAAGGCCATCATCATCACCCGTGTGGGTCAATC 480

Db 421 TACAACCTGAAGCGCACGCCGCGCATCAAGGCCATCATCATCACCCGTGTGGGTCAATC 480

QY 481 TCGGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGGCGCGGCGCGGC 540

Db 481 TCGGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGGCGCGGCGCGGC 540

QY 541 CCGCAGCCGCGGAGCGCGGCTCGAGATCAACGACCAGAGTGGTACGTCACTCTCGTCG 600

Db 541 CCGCAGCCGCGGAGCGCGGCTCGAGATCAACGACCAGAGTGGTACGTCACTCTCGTCG 600

QY 601 TGCATCGGCTCCTTCTTCGCTCCCTGCCTCATCATGATCTCTGGTCTACGTGCGCATCTAC 660

Db 601 TGCATCGGCTCCTTCTTCGCTCCCTGCCTCATCATGATCTCTGGTCTACGTGCGCATCTAC 660

QY 661 CAGATCGCCAAAGCGTCGCACCCGCGTGCCACCCAGCGGCCCGGGGTCCGGACGCCGTCGCC 720

Db 661 CAGATCGCCAAAGCGTCGCACCCGCGTGCCACCCAGCGGCCCGGGGTCCGGACGCCGTCGCC 720

QY 721 GCGCCGCGGGGGGACCCGAGCGCAGGCCCAACGGTCTTGGGCCCGGAGCGAGCGCGGGC 780

Db 721 GCGCCGCGGGGGGACCCGAGCGCAGGCCCAACGGTCTTGGGCCCGGAGCGAGCGCGGGC 780

QY 781 CCGGGGGGCGCAGAGCGCGAACCCGCTGCCACCCAGCTCAACGGCGCCCTTGGCGAGGCC 840

Db 781 CCGGGGGGCGCAGAGCGCGAACCCGCTGCCACCCAGCTCAACGGCGCCCTTGGCGAGGCC 840

QY 841 GCGCCGCGGGCGCGCGGACACCGACCGCGCTGGACCTGGAGGAGAGCTCGTCTTCCGAC 900

Db 841 GCGCCGCGGGCGCGCGGACACCGACCGCGCTGGACCTGGAGGAGAGCTCGTCTTCCGAC 900

QY 901 CACGCCGAGCGGCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCCGGGGCAAGGCAAG 960

Db 901 CACGCCGAGCGGCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCCGGGGCAAGGCAAG 960

QY 961 GCCCGAGCGCAGGTGAAGCCGGCGCAGACCTGCCCGCGCGGGCGGGCGGGCGGACG 1020

Db 961 GCCCGAGCGCAGGTGAAGCCGGCGCAGACCTGCCCGCGCGGGCGGGCGGGCGGACG 1020

QY 1021 GGGATCGGACCGCGGCTGCAGGCGCGGGGAGGAGCGCGTGGGGGTGCCAAGCGTCG 1080

Db 1021 GGGATCGGACCGCGGCTGCAGGCGCGGGGAGGAGCGCGTGGGGGTGCCAAGCGTCG 1080

QY 1081 CGCTGGCGGGCGGCGAGAACCGCGAGAACGCTTACGTTCTGTGTCGTCGTCATC 1140

Db 1081 CGCTGGCGGGCGGAGAACCGGAGAGCGCTTCACGTTCTGCTGGCCGTTGGTTCATC 1140
QY 1141 GGAGTGTTCGTGGTGTCTGGTTCCTCCCTTCTTCTTACCTACACGCTCACGGCCGTCGGG 1200
Db 1141 GGAGTGTTCGTGGTGTCTGGTTCCTCCCTTCTTCTTACCTACACGCTCACGGCCGTCGGG 1200
QY 1201 TGCTCCGTGCCACGACGCTCTTTCAAATTCTTCTGGTTCGGCTACTGCAACAGCTCG 1260
Db 1201 TGCTCCGTGCCACGACGCTCTTTCAAATTCTTCTGGTTCGGCTACTGCAACAGCTCG 1260
QY 1261 TTGAACCCGGTTCATACACCATCTTTCAACACAGGATTTCCGCCCGGCTTCAAGAAGATC 1320
Db 1261 TTGAACCCGGTTCATACACCATCTTTCAACACAGGATTTCCGCCCGGCTTCAAGAAGATC 1320
QY 1321 CTCTGTGGGGGACAGGAAGCGGATCGTG 1350
Db 1321 CTCTGTGGGGGACAGGAAGCGGATCGTG 1350

RESULT 3
ABQ47500/c
ID ABQ47500 standard; DNA; 1733 BP.
XX ABQ47500;
AC
XX
DT 12-JUL-2002 (first entry)
XX
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34091.
XX
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX

OS Homo sapiens.
XX
XX WO200218632-A2.
PN
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EPI0074.
XX
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.

XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the

CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0 other;
Query Match 67.9%; Score 917; DB 24; Length 1733;
Best Local Similarity 80.0%; Pred. No. 1.3e-135;
Matches 1079; Conservative 0; Mismatches 270; Indels 0; Gaps 0;
QY 1 ATGGGCTCCCTGCAGCCGGACGGGGCAACGCGAGCTGGAACGGGACCGAGGCCCGGG 60
Db 1473 ATAAACTCCCTACAACCGAACGCGAACTAAACGCGAACTAAACGCGAAACCGCGAAA 1414
QY 61 GCGGGCGCCCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCC 120
Db 1413 AACGACGCCCGAACCCCTTACTCCCTACAAATAACGCTAACGCTAATATACCTAAC 1354
QY 121 GGCCTGCTCATGCTGCTCACCGTGTTCGGCAACGCTGCTCGTCATCATCGCCGTTCACG 180
Db 1353 GACCTACTCATACTACTACCGTATTTCGACAACGTACTCGTCATCATCGCCGTATTACG 1294
QY 181 AGCCGCGCGCTCAAGCGGCCCCCAAAACCTTCTCTGGTGTCTCTGGCTCGGCCGACATC 240
Db 1293 AACCGCGCGCTCAAAACGCCCCCAAAACCTTCTCTAATATCTCTAACCTCGACCGACATC 1234
QY 241 CTGGTGGCCACGCTCGTCATCCCTTTCTCGTGGCCCAACGAGGTATGGGCTACTGGTAC 300
Db 1233 CTAATAACCAACGCTCGTCATCCCTTTCTCGTTAAACCAACGAAATCATAAACTACTAATAC 1174
QY 301 TTCGGCAAGGCTTGGTGGAGATCTACCTGGCGCTGACGCTGCTCTTCTGCACGTCGTCC 360
Db 1173 TTCGACAAAACCTTAATACGAAATCTACCTAAGCTCGACGTACTCTTCTACACGTCGTCC 1114
QY 361 ATCGTGCACTGTGCGCCATCAGCCTGGACCGTACTGGTCCATCACACAGGCCCATCGAG 420
Db 1113 ATCGTACACCTATACGCCATCAACCTTAAACCGTACTAATCCATCACACAAACCATCGAA 1054
QY 421 TACAACTGAAGCGCACCGCCGCGCATCAAGGCCATCATCATCACCGTGTGGTTCATC 480
Db 1053 TACAACTTAAACGCGACCGCGCGCATCAAAACCATCATCATCACCGTATAAATCATC 994
QY 481 TCGGCCGTCACTCTCTTCCGCGCTCATCTCCATCGAGAAAGGGGCGCGCGCGCGC 540
Db 993 TCGACCGTCATCTCTCTTCCGCGCTCATCTCCATCGAAAAAACAACGACGACGAC 934
QY 541 CCGACGCGCGCGAGCGCGCTGCGAGATCAACGACCAAGAGTGGTACGTCACTCTCGTCG 600
Db 933 CCGCAACCGACCGCAACCGCGCTACGAAATCAACGACCAAAATAATACGTCACTCTCGTCG 874
QY 601 TGCATCGGCTCCTTCTCGCTCCCTGCTCATCATGATCCTGGTCTACGTGCGCATCTAC 660
Db 873 TACATCGACTCCTTCTTCCGCTCCCTACCTCATCATATAATCCTAATCTACGTACGTCATC 814
QY 661 CAGATCGCCAAAGCGTCGACCCCGCTGCCACCCACCGCGGGTCCGGACGCGCGTCGCGC 720
Db 813 CAAATCGCCAAACGTCGACCCCGGTACCCACCCACCGCGGAAATCCGAAACGCGCGTCGCC 754
QY 721 GCGCGCGCGGGGACCGAGCGCAGGCCCAACCGGTCTGGGCCCCCGAGCGCAGCGCGGC 780
Db 753 GCGCGCGCGGAAAAACCGAACGCAACCCCAACGATCTAAACCCCGAACGCAACGCGAAC 694
QY 781 CCGGGGGCGCAGAGGCGGAACCGCTGCCACCCAGCTCAACGGGCGCCCCCTGGCGAGCCCC 840
Db 693 CCGAAAAACGCAAAAAACCGAACCGCTACCCACCCCACTCAACGACGCGCCCTAACGAACCC 634
QY 841 GCGCGCGCGGGCGCGCGACACCGCTGCCACCCAGCTCAACGGGCGCCCCCTGGCGAGCCC 900
Db 633 GCGCGCGCGGAACCGCGCGACACCGACGCGCTAAACCTAAAAAATACTCGTCTTCCGAC 574
QY 901 CACGCGGAGCGGCTCCAGGGCCCCGACAGACCCGAGCGCGGTCCCCGGGCAAGCAAG 960

Db 981 GCGCCGCGGAAAAACACCGAACGCGAAACCCCAACGATCTAAACCCCGAAGCAACGCGAAC 1040

QY 781 CCGGGGGCGCAGAGGCGGACCGCTGCCCCACCCAGCTCAACGGCGCCCTGGCGAGCCC 840

Db 1041 CCGAAAAACGAAAAACCGAACCGCTACCCACCCAACTCAACGACGCCCTTAACGAACCC 1100

QY 841 GCGCCGCGCGCGCGCGGACACCGACCGCGCTGGACCTGGAGGAGAGCTCGTCTTCGAC 900

Db 1101 GCGCCGACCGAACCGCGCGGACACCGACCGCGCTAAACCTAAAAAAAACCTCGTCTTCGAC 1160

QY 901 CACGCGAGCGGCTCCAGGGCCCCGACAGCCCGAGCGCGTCCCCGGGGCAAGGCAAG 960

Db 1161 CACGCGAACGACCTCCAAAACCCCGCAAAACCCGAACCGGATCCCCGAAACAAAAACAAA 1220

QY 961 GCCCGAGCGAGCCAGGTGAAGCCGGCGACAGCCTGCCGCGCGCGCGCGCGGCGGACG 1020

Db 1221 ACCGGAACGACCAAAATAAAACCGAACGACAACCTACCGGACGCGGAACCGAAAAACGAG 1280

QY 1021 GGGATCGGGACCGCGGCTGCAGGGCCCCGGGAGGAGCGCGTCCGGGCTGCCAAGCGTCG 1080

Db 1281 AAAATCGAAACGCGACTACAAAACCGAAAAAAAACGCGTCGAAACTACCAAAACGTCG 1340

QY 1081 CGCTGGCGCGGCGGAGAACCGCGAGAGCGCTTACAGTTCTGCTGGCGCGTGGTTCATC 1140

Db 1341 CGCTAACCGGAACGACAAAAACCGGAAAAACGCTTACGTTCTGTAATAACCGTAATCATC 1400

QY 1141 GGAGTGTTCGTGGTGTGCTGGTCCCTTCTTTCACCTACACGCTCACGGCCGTCGGG 1200

Db 1401 GAAATATTCTGTAATATACTAATTCCCTTCTTCTTCACTACACGCTCACGACCGTCGAA 1460

QY 1201 TGCTCCGTGCCACGACGCTCTTCAAATTTCTTCTGGTTTGGCTACTGCAACAGCTCG 1260

Db 1461 TACTCCGTACCACGACGCTCTTCAAATTTCTTCTTAATTCGACTACTACAACAACCTCG 1520

QY 1261 TTGAACCCGGTCACTACACCATCTTCAAACCAAGATTTCCGCCGCGCTTCAAAGAAGATC 1320

Db 1521 TTAACCCGATCATCTACACCATCTTCAAACCAAGATTTCCGCCGCGCTTCAAAAAAATC 1580

QY 1321 CTCTGTCCGGGGACAGGAACGGGATCGT 1349

Db 1581 CTCTATCGAAAAACAAAAACGAATCGT 1609

RESULT 5

ABL32073/c

ID ABL32073 standard; DNA; 7353 BP.

XX ABL32073;

AC ABL32073;

XX 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 46.

DE Human; immune system disease; cytosine methylation; antiasthmatic;

XX Human; immune system disease; cytosine methylation; antiasthmatic;

KW antiarteriosclerotic; antianaemic; cytosine methylation; antiasthmatic;

KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;

KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

KW gene; ds.

XX Homo sapiens.

OS Homo sapiens.

XX WO200200928-A2.

PN 03-JAN-2002.

XX 02-JUL-2001; 2001WO-EP07537.

PF 30-JUN-2000; 2000DE-1032529.

XX 01-SEP-2000; 2000DE-1043826.

PR

XX

PA (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

PI WPI; 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful

PT for diagnosis and treatment of diseases associated with abnormal

PT cytosine methylation -

XX Claim 1; SEQ ID NO 46; 32pp + Sequence Listing; German.

PS The present invention provides a number of human immune system associated

XX genes which are modified by the methylation of cytosines. The sequences

CC can be used in the diagnosis and treatment of immune system disorders,

CC including eye diseases such as retinopathy, neovascular glaucoma and

CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel

CC diseases. The present sequence is a gene of the invention.

XX Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

SQ

Query Match 67.9%; Score 917; DB 24; Length 7353;

Best Local Similarity 80.0%; Pred. No. 1.2e-135;

Matches 1079; Conservative 0; Mismatches 270; Indels 0; Gaps 0;

QY 1 ATGGGCTCCCTGCAGCCGACGCGGGCAACGCGAGCTGGAACGGGACGAGCGCCGGG 60

Db 2353 ATAAACTCCCTACACCGAACGGAACAACGGAACCTAAACGGAACCGAAACGCGAAA 2294

QY 61 GCGGCGCGCGCGGCGGACCGCTTACTCCCTGAGGTGACGCTGAGCTGGTGTGCCTGGCC 120

Db 2293 AACGACGCGCGAACCGGCGGCTTACTCCCTACAAATAACGCTAACGCTAATATACCTAAC 2234

QY 121 GGCCTGCTCATGTGCTACCGGTGTTTCGGCAACGCTGCTCGTCATCATCGCCGTGTCACG 180

Db 2233 GACCTACTCATACTACTACCGTATTTCGACACGTAATCGTATCATCGCCGTATTCACG 2174

QY 181 AGCGCGCGCTCAAGGCG 240

Db 2173 AACCGCGCGCTCAAAACG 2114

QY 241 CTGTGGCCACGCTCGTCAATCCCTTTCTCGTGGCGCGCGCGCGCGCGCGCGCGCGCG 300

Db 2113 CTAATAACCGCTCGTCAATCCCTTTCTCGTAAACCGCGCGCGCGCGCGCGCGCGCGCG 2054

QY 301 TTCGCAAGGCTTGGTGCAGATCTACCTGGCGCTGAGCGCTGCTGCTGCTGCTGCTGCT 360

Db 2053 TTCGCAAAACTTAATACGAAATCTACCTAACGCTGAGCGTACTCTTCTACAGCTCGTC 1994

QY 361 ATCTGACCTGTGCGCCATCAGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCGCGCGCG 420

Db 1993 ATCTGACCTTATACGCGCTCAACCTAAACCGCTACTAATCCATCACACAAACCATCGAA 1934

QY 421 TACAACCTGAAGCG 480

Db 1933 TACAACCTGAAGCG 1874

QY 481 TCGGCGCTCATCTCTTTCGGCGCTCATCTCCATCGAAGAGAGGGCGCGCGCGCGCGCG 540

Db 1873 TCGACCGCTCATCTCTTTCGGCGCTCATCTCCATCGAAGAGAGGGCGCGCGCGCGCG 1814

QY 541 CCGCAGCG 600

Db 1813 CCGCAACCG 1754

QY 601 TGCATCGGCTCTCTTTCGGCTCCCTGCTCATCATGATCCTGCTGCTGCTGCTGCTGCT 660

Db 1753 TACATCGACTCTCTTTCGGCTCCCTACCTCATCATATAATCTAATCTACGTACGCTAC 1694

QY 661 CAGATCGCGCAAGCGTTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720


```
QY 421 TACAACCTGAAGGCACGCGCGCGCATCAAGCCATCATCATCACCGTGTGGTCAATC 480
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 681 TATAATTTGAAGCGTACGTCGCGTCGTAATAAGTTATTATTATATCGTGTGGTTATT 740

QY 481 TCGGCGGTCAATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGCGGCGGCGGC 540
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 741 TCGGTCTGTTATTTTTCGTCTGTTTATTATCGAAGAGGCGGCGGCGGCGGT 800

QY 541 CCGCAGCGCGCGAGCGCGCTCGAGATCAACGACCAGAAAGTGTACGTCACTCTCG 600
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 801 TCGTAGTCGGTCGAGTCGCTTTCGAGATTAAAGATTAGAAAGTGTACGTTATTTCTCG 860

QY 601 TGCATCGGCTCCTTCTTCGCTCCCTGCTCATCATGATCCTGGTCTACGTGCGCATCTAC 660
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 861 TGTATCGGTTTTTTTCGTTTTTGTATTATATGATTTTGGTTACGTGCGTATTAT 920

QY 661 CAGATCGCAAGCGTCGACCCCGCTGCCACCCAGCCCGCGGCTCCGACGCGCTCGCC 720
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 921 TAGATCGTTAAGCGTCGTATTTCGCTGTTATTAGTCGTCGGGTTTCGACGTCGTCGTC 980

QY 721 GCGCCCGCGGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCGAGCGCAGCGCGGC 780
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 981 GCGTCGTCGGGGGTATCGAGCGTAGGTTTAAACGGTTTGGGTTTCGAGCGTAGCGCGGT 1040

QY 781 CCGGGGGCGCAGAGCGCGAACCCTGCCCCAGCTCAACGGCCCCCTGGCGAGCCCC 840
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1041 TCGGGGGCGTAGAGGTCGAATCGTTTATTATTAGTTTAAACGGGTTTTTGGCGAGTTC 1100

QY 841 GCGCCCGCGGGCGCGCACCCGACCGCGCTGGACCTGGAGAGAGCTCGTCTTCGAC 900
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1101 GCGTCGTCGGGTCGCGCATATCGACGCTTGGATTTGGAGAGAGTTCGTTTTTCGAT 1160

QY 901 CAGCGCAGCGGCTCCAGGGCCCCGCGACAGCCGAGCGCGTCCCGGGGCAAGCAAG 960
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1161 TACGTCGACGCGTTTTTAGGGTTTCGTAGATTCGAGCGCGTTTTTCGGGTTAAAGTAAG 1220

QY 961 GCCCGAGCGCAGGTGAAGCCGGGCGACAGCCTGCCGCGCGCGGCGCGGCGACG 1020
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1221 GTTCGAGCGAGTTAGGTGAAGTCGGGCGATAGTTTGTGCGGCGCGGTCGCGGCGACG 1280

QY 1021 GGGATCGGACCGCGGTGACGGCGGGGAGGAGCGCGTCCGCGGCTGCCAAGCGTCG 1080
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1281 GGGATCGGACGTCGTTGTAGGTTCGGGGAGGAGCGCGTCCGCGGTTGTTAAGCGTCG 1340

QY 1081 CGCTGGCGCGGCGGAGAACCCGAGAACGCTTCACGTTCTGCTGGCGCGTGCATC 1140
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1341 CGTTGGCGCGGCGGTAGAAATCGCAGAACGTTTTACGTTCTGTTGGTCTGCGTTATC 1400

QY 1141 GGAGTGTCTGGTGTCTGTTCCCTTCTTCACTACAGCTACAGCTACAGCGCGTCGGG 1200
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1401 GGAGTGTCTGGTGTCTGTTTGTGTTTTTTTTTTTATTATACGTTTACGCGTCTCGG 1460

QY 1201 TGCTCGTGCCACGACGCTCTCAAAATCTTCTTCTGGTTCGGCTACTGCAACAGCTCG 1260
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1461 TGTTCTGTGTACGTACGTTTTTTTAAATTTTTTTTTTGGTTCGTTATTGTAATAGTTCG 1520

QY 1261 TTGAACCCGGTCACTACACCAATCTTCAACACGATTTCCGCGCGCTTCAAGAAGATC 1320
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1521 TTGAATCGGTTATTTATATATTATTAAATACGATTTTCGTCGCGTTTTTAAAGAAATT 1580

QY 1321 CTCTGCGGGGGACAGGAAGCGGATCGTG 1350
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1581 TTTTGTGCGGGGGATAGGAAGCGGATCGTG 1610
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 8
ABQ47499/c
ID ABQ47499 standard; DNA; 1733 BP.
XX
AC ABQ47499;
XX
DT 12-JUL-2002 (first entry)
```

```
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34090.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA _
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 685 A; 585 C; 211 G; 252 T; 0 other;
```

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Query Match 62.1%; Score 838; DB 24; Length 1733;
Best Local Similarity 76.3%; Pred. No. 3.2e-123;
Matches 1030; Conservative 0; Mismatches 320; Indels 0; Gaps 0;

QY 1 ATGGGCTCCCTGCAGCCGGACGCGGGCAACGCGAGCTGGAACGGACCGAGGCGCGGGG 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1473 ATGGGTTTTTTGTAGTCGGACGCGGGTAACGCGAGTTGGAACGGGATCGAGGCGTCGGG 1414

QY 61 GGCGGCGCGCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTCCCTGSCC 120
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1413 GGCGGCGTTCGGGTTATTTTTTATTTTTTGTAGGTGACGTTGCTGTTGTTGTC 1354

QY 121 GGCCTGCTCATGCTGCTCACCCTGTTTCGGCAACGCTGCTCGTCATCATCGCCGTTACG 180
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1353 GGTTCGTTATGTTGTTTATCGTGTTCGGTAACGTTTCGTTATTCGTCGTTTACG 1294

QY 181 AGCCGCGCGCTCAAGGCGGCCCAAAACCTCTTCTGTTGTTCTCTGGCCTCGGCCGACATC 240
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1293 AGTCGCGCGGTTTAAGGCGGTTTTTAAAAATTTTTTTTTTGGTGTGTTTTCGTCGATATT 1234
```


CC	positions 961-972 of (III). The method may be used for genotyping an
CC	alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC	whether an individual is at increased risk of developing a disease
CC	associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC	polymorphic site which correlate to disease selected from cardiovascular
CC	disease, central nervous system disease and combinations of these. In
CC	addition, the technique may be used to predict an individual's response
CC	to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC	norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC	combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC	rauwolscine, idazoxan, tolazoline, phentolamine and combinations of
CC	these) by detecting the polymorphic site and correlating the site to a
CC	predetermined response (where the response is correlated to adenylyl
CC	cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC	levels). The present sequence is that of the human alpha-2CAR, the
CC	sequence includes a 12 nucleotide polymorphic site at nucleotides
CC	961-972, absent in the alpha-2CAR variant (AAI99933).
XX	
SQ	Sequence 1383 BP; 164 A; 482 C; 500 G; 237 T; 0 other;
	Query Match 39.3%; Score 530.6; DB 23; Length 1383;
	Best Local Similarity 65.4%; Pred. No. 5.6e-75;
	Matches 876; Conservative 0; Mismatches 419; Indels 44; Gaps 5;
QY	19 GACGCGGGCAACGCGAGCTGGAAACGGGACCGAGCGCGCGGGGGCGCGCCCGGGCCACC 78
DB	73 GAGAGGGCAGCGCGGGGTTGCCAATGCCTCGGGGGCTTCTGGGGCGCGCGCGCGGC 132
QY	79 CCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCTGCGCGCGCTGCTCATGTGCTC 138
DB	133 CAGTACTCGGCGGCGCGGTGGCAGGGCTGGCTGCCGTGGTGGCTTCTCATGCTCTTC 192
QY	139 ACCGTGTTTCGGCAACGTGCTCGTCATCATCGCCGTGTTACGAGCGCGCGCTCAAGGCG 198
DB	193 ACCGTGTTGGCAACGTGCTGGTGGTATCGCCGTGCTGACCAAGCGCGCGCGCGCG 252
QY	199 CCCCAGAAACCTCTTCTCTGGTGTCTCTGGCCTCGGCCGACATCCTGGTGGCCACGCTCGTC 258
DB	253 CCACAGAACCTCTTCTCTGGTGTGCTGGCCTCGGCCGACATCCTGGTGGCCACGCTGGTC 312
QY	259 ATCCCTTTCTCGTGGCCAACGAGGTGATGGGCTATGGGTACTGTGCTACCTCGGCAAGGTTGGTGC 318
DB	313 ATGCCCTTCTCGTTGGCCAACGAGCTCATGGCCTACTGGTACTTTCGGGCAGGTGGTGC 372
QY	319 GAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACTGCTCCATCGTGACCTGTGCGCC 378
DB	373 GCGGTGTACCTGGCGCTCGATGTGCTGTTTGCACCTCGCTCGATCGTGCATCTGTGTGCC 432
QY	379 ATCAGCCTGGACCGCTACTGTGTCATCACACAGGCCATCGAGTACAACCTGAAGCGCACG 438
DB	433 ATCAGCCTGGACCGCTACTGTGCTGACGCGAGCCCTCGAGTACAACCTGAAGCGCAC 492
QY	439 CCGCGCGCATCAAGGCCATCATCATCCGCTGTGGTTCATCTCGGCCGCTCATCTCCTTC 498
DB	493 CCACGCGCGCTCAAGGCCACCATCGTCGCGGTGTGGTTCATCTCGGCCGCTCATCTCCTTC 552
QY	499 CCGCGCGCTCATCTCCATCGAGAAGAAGGGCGGGCGGGCGGCCCGCAGCGCGCGGAGCCG 558
DB	553 CCGCGCGTGGTCTCGCTCTACCGCCAGCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
QY	559 CGCTGCGAGATCAACGACGAGAGTGGTACGTATCTCTGCTGCTGCTGCTGCTGCTTCTTC 618
DB	601 CAGTGGCGGCTCAACGACGAGACCTGGTATCATCTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY	619 GCTCCCTGCTCATCATGATCTGCTGCTACGTGGCATCTACCGATCGCCAAAGCGTCCG 678
DB	661 GCGCCCTGCTCATCATGGGCTGGTCTACGCGCGCATCTACCGAGTGGCCAAAGCGTCCG 720
QY	679 ACCCGCGTGCCACCCAGCCCGGGGTCCGGACGCGGTGCGCGCGCGCGCGGGGGGACCC 738
DB	721 ACGCGCAGCTCAGCGAGAAGCGCGCCCCCGTGGGCCCCGACGGTGGCTCCCCGACTACC 780
QY	739 GAGCGCAGGCCCAACGGTCTTGGGCCCCCGAGCGCGCGGGCGCGGGGGGGCGCAGAGGCC 798

DB	781 GAAACCGGCTGGCGCGCGCGAGCGGAGGCGAGAACCGGCACTGCGCGC----- 831
QY	799 GAACCGCTGCCACCCAGCTCAACGGCGGCCCTTGGCGAGC-CCGGCGCGCGCGGCGCGCG 857
DB	832 -----CCCGCGCGCGCGACGTGGAGCGCGGACGAGAGCAGCGAGCGCGCGGAGGCG 883
QY	858 CGACACCGACCGGCTGGACCTTGAGGAGAGCTCGTCTTCCGACCAACGCGCGGCGCTCC 917
DB	884 GCGCGCGGGGCGGCTTGGCGGGGGCGGGCGGCGAGCGGGCGCGGAGGGGGCGCGG 943
QY	918 AGGCGCGCGCAGACCCGAGCGCGGTCCCGGGGGCAAAGGCAAGGCCCGAGCGAGCCAGGT 977
DB	944 GCGGTGCGGACGGGCGGGGGCGGGGGCGGGGGCGGCTGAGTCGGGGCGCTGACCGCCT 1003
QY	978 GAAGCCGGGCGACAGCCTGCCCGCGCGGGCGGGCGGGGGCGGAGATCGGGACCGCGG 1037
DB	1004 CCAGGTCCCCGGGGCGGTTGGCCCGCTCTCGCGCGCCAGCTCGCGCTCCGTCGAGTTCT 1063
QY	1038 TGCAGGGCGGGGAGGAGCGCGTGGGGGCTGCCAAGCGCTGCGCGTGGCGGGCGGCA 1097
DB	1064 TCCTGTGCGCGCGCGCGCGCGCGGCGGCGAG-----CAGCGTGTGCGCGCGCAAGGTGGCCCA 1118
QY	1098 GAACCGCGAGAACGCTTACAGTTCTGCTGGCTGGCGGTGGTCAATCGGAGTGTTCGTGGTGTG 1157
DB	1119 GCGCGCGGAGAACGCTTACCTTGTGCTGGCTGTGGTCAATCGGCGTGTTCGTGCTCTG 1178
QY	1158 CTGTTCCCTTCTTCTTACCTACACGCTCACGGCGCTC-----GGGTGCTCCGT 1208
DB	1179 CTGTTCCCTTCTTCTTATCTACAGCCTGTACGGCATCTGCCGCGAGGCTGCCAGGT 1238
QY	1209 GCCACGCAAGCTTCAAATCTTCTTCTGTTGGTTCGGCTACTGCAACAGCTCGTTGAACCC 1268
DB	1239 GCCCGCGCGCTCTTCAAGTTCTTCTTCTGATCGGCTACTGCAACAGCTCGTCAACCC 1298
QY	1269 GGTCACTTACACCATCTTCAACCAACGATTTCCGCGCGGCTTCAAGAAGATCCTCTGTG 1328
DB	1299 GGTCACTTACAGGCTTCAACCAACGATTTCCGCGCATCTTCCGCGCATCTTCAAGCACATCTCTTCCG 1358
QY	1329 GGGGACAGGAAGCGGATC 1347
DB	1359 ACGGAGAGAGGGGCTTC 1377
RESULT 12	
AAI99933	
ID	AAI99933 standard; DNA; 1371 BP.
XX	
AC	AAI99933;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Human alpha-2CAR variant encoding DNA.
XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.
OS	Homo sapiens.
XX	
FH	Key
CDS	Location/Qualifiers
FT	1..1371
FT	/*tag= a
FT	/product= "alpha-2CAR"
FT	/note= "sequence is deleted for a 12 nucleotide
FT	polymorphic site at nucleotides 961-972 of the
FT	wildtype sequence (AAI99931)"
XX	
PN	WO200179561-A2.
XX	
PD	25-OCT-2001.
XX	

PF 17-APR-2001; 2001WO-US12575.
XX 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX (LIGGETT) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX Liggett SB, Small KM;
XX WPI; 2001-611728/70.
DR P-PSDB; AAM52126.
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX Claim 103; Page 158; 163pp; English.
PS The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2CAR variant,
CC the sequence is deleted for a 12 nucleotide polymorphic site at
CC nucleotides 961-972 of the wildtype gene (AAI99931).
XX
SQ Sequence 1371 BP; 164 A; 479 C; 491 G; 237 T; 0 other;
Query Match 38.3%; Score 517.6; DB 23; Length 1371;
Best Local Similarity 65.0%; Pred. No. 6.2e-73;
Matches 870; Conservative 0; Mismatches 414; Indels 54; Gaps 5;
QY 19 GACGCGGGCAACGGAGCTGGAACGGGACCGAGGCGCGGGGGGGCGCGCGCGCGCCACC 78
DB 73 GAGAGGGGCGAGCGCGGGGTGCCAATGCCTCGGGGGCTTCCTGGGGGGCGCGCGCGC 132
QY 79 CATTACTCCCTGCAGGTGACGTGACGTGGTGTGCTGGCGCGCGCGCTGCTATGCTGCTC 138
DB 133 CAGTACTCGGGGGCGCGCGGTGGAGGGCTGGTGGCGGTGGGTGGGTTCCTCATGCTCTTC 192
QY 139 ACCGTGTTCCGCAACGTGCTCGTCATCATCGCGGTGTTCACGAGCCGCGCGCTCAAGGCG 198
DB 193 ACCGTGTTGGCAACGTGCTGGTGTGATCGCGGTGATCGCGGTGATCGAGCCGCGCGCGCG 252
QY 199 CCCCCAAACCTCTTCTCTGTGTCTGTGGCGCTCGGCCGACATCCTGGTGGCCACGCTCGTC 258
DB 253 CCACAGAACCTCTTCTCTGTGTGCTGGCGCTCGGCCGACATCCTGGTGGCCACGCTGGTC 312
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DB 313 ATGCCCTTCTCGTTGGCCCAACGAGTCACTGGCTACTGGTACTTCGGGCAGGTGTTGCTGC 372
QY 319 GAGATCTACTGGCGCTCGACGTGCTTCTTGCACGTGCTGCCATCGTGACCTGTGCGCC 378

Db 373 GGCGTGTACTGGCGCTCGATGTGCTGTTTGGACCTCGTCGATCGTGCATCTGTGTGCC 432
QY 379 ATCAGCCTGGACCGCTACTGTGCATCACACAGGCCATCGAGTACAACCTGAAGCGCACG 438
Db 433 ATCAGCCTGGACCGCTACTGTGTCGTCAGCGCGCTGAGTACAACCTGAAGCGCAC 492
QY 439 CCGCGCGCATCAAGGCCATCATCATCACCGTGTGGTTCATCTCGGCCGTATCTCTTC 498
Db 493 CCAGCGCGGTCAAGGCCACCATCGTCGCGGTGTGGTTCATCTCGGCCGTATCTCTTC 552
QY 499 CCGCGCTCATCTCCATCGAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
Db 553 CCGCGCTGGTCTCGCTCTACCGCCAGCCCGACGCGG-----CCGCTACCCG 600
QY 559 CGTGGAGATCAACGACCAAGTGTGTACGTCTCTCGTCGTGTCATCGGCTCCTTCTTC 618
Db 601 CAGTGGCGCTCAACGACGAGACCTGTGTACATCTCTCTCTCGTCATCGGCTCCTTCTTC 660
QY 619 GCTCCCTGCTCATCATGATCTGTGTCTACGTGCGCATCTACAGATGCCAAGCGTCGC 678
Db 661 GCGCCCTGCTCATCATGGGCTGGTGTACGCGCGCATCTACGAGTGGCAAGCGTCGC 720
QY 679 ACCGCGTGCACCCAGCCGCGGGTTCGGACCGCTCGCGCGCGCGCGCGCGCGCGCGCC 738
Db 721 ACGCGACGCTCAGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 739 GAGCGCAGCCCAACCGTCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 798
Db 781 GAAACGGGCTGGCG 827
QY 799 GAACCGCTGCCACCCAGCTCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 858
Db 828 GCGCCCCCG 887
QY 859 GACACCGACCGCTGGACCTGGAGGAGAGTCTCTTCCGACCGCGCGCGCGCGCGCG 918
Db 888 GCGGGGCGCTTGGCG 935
QY 919 GGGCCCCCGCAGACCCGAGCGCGGTTCGCCGGGCAAGGCAAGCCCGAGCGAGCGAGTG 978
Db 936 GGGCGCGCGCGGTGCGGACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 995
QY 979 AAGCGCGCGCAGACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1038
Db 996 GTCCCGGGGCGCGGTGCGCGCGCGCTCTCGCGCGCGCGCGCGCGCGCGCGCGCG 1055
QY 1039 GCAGGGCGGGGAGGAGCGCGTGGGGGTGCCAAGCGCGTCCGCGTGGCGCGCGCGCAG 1098
Db 1056 GTCGCGCGCGCGCGCG-----GCGCGCAGCAGCGTGTGCCCGCGCAAGGTGGCC 1107
QY 1099 AACCGCGAGAACGCTTCACTGCTGCTGGCGGTGTCATCGGAGTGTGCTGCTGTC 1158
Db 1108 GCGCGCGAGAACGCTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
QY 1159 TGGTCCCTTCTTCTTCACTACCGCTCACGCGTCCGCGCGT-----GGGTGCTCCGTG 1209
Db 1168 TGGTCCCTTCTTCTTCACTACCGCTTACGCGTGTACGCGCATCTCGCGGAGCGCTG 1227
QY 1210 CCACGACGCTCTTCAATCTTCTTCTGTTTCCGTTACTGCAACAGCTCGTTGAACCCG 1269
Db 1228 CCGCGCGCGCTCTTCAAGTCTTCTTCTGATCGGCTACTGCAACAGCTCGCTCAACCCG 1287
QY 1270 GTCATCTACACCATCTTCAACACGATTTCCGCGCGCGCTTCAAGAAGATCTCTGTGCG 1329
Db 1288 GTCATCTACACGCTTCAACACGAGATTTCGCGCGCGCTTCCGGCCATCTTCAAGCACAT 1347
QY 1330 GGGGACAGGAAGCGGATC 1347
Db 1348 CGAGGAGAGAGGGGCTTC 1365
RESULT 13

Db 606 CAACCGCAGAGGTCCAGGGCCAAAGGG--GGGGCCTGGCAGGGTGAGTCCAAGCAGCCCC 663

QY 738 CGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCGCAGCGGGGCCCGGGG-----GGCGCA 792

Db 664 CGACCCGACCATGGTGGGGCTTTGGGCTCAGCCAAACTGCCAGCCCTGGCCTCTGTGGCT 723

QY 793 GAGGCCGAACCGCTGCCACCCAGCTCAACGGGCCCTTGGGAGCCCGCGCCGCGGG 852

Db 724 TCTGCCAGAGAGGTCAACGGACACTCGAAGTCCACTGGGAGAAAGGAGGGGGAGACC 783

QY 853 CCGCGCGACACCGACGCGCTGGACCTGGAGGAGAGCTCGTCTTCGACCACCGCCGAGCGG 912

Db 784 CCTGAAGATACTGGGACCCGGGCTTGCCACCCAGTTGGGCTGCCCTTCCCAACTCAGGC 843

QY 913 C-----CTCCAGGGCCCCGACACCCCGAGCGCG 940

Db 844 CAGGGCCAGAAGAGGGTGTTTGTGGGGCATCTCCAGAGGATGAAGCTGAAGAGGAGGAG 903

QY 941 GTCCCCGGGCAAAAGCAAGGCCCGAGCCAGCCAGGTGAAGCCGGGCGACAGCCTGCCGC 1000

Db 904 GAGGAGGAGGAAGAGTGTGAACCCAGCCAGGAGTGCCAGTGCTCCGGCCTCAGCTTGACG 963

QY 1001 GGCGCGGCGCGGGCGGACGGGATCGGG-----ACGCCGGTGCAGGGC 1045

Db 964 CCCCCGCTGCAGCAGCCACAGGGCTCCCGGTGCTGGCCACCCCTACGTGGCCAGGTGCTC 1023

QY 1046 CGGGGAGGAGCGCGTCGG---GGCTGCCAAGGCGTCCGCTGGCGCGGGCGGCAGAAC 1101

Db 1024 CTGGGCAGGGCGTGGGTGCTATAGGTGGCAGTGGTGGCGTCGAAGGGCGCAGCTGACC 1083

QY 1102 CGCGAGAAGCGCTTCACGTTCTGCTGGCGGTGGTTCATCGGAGTGTTCGTGGTGTGCTGG 1161

Db 1084 CGGGAGAAGCGCTTCACCTTCGTCTGGCTGGTGTGGTCAATTGGCGTTTGTGCTCTGCTGG 1143

QY 1162 TTCCCTTCTTCTTCACTACAGCTCACGGCCGTCGG-----GTGCTCCGTGCCA 1212

Db 1144 TTCCCTTCTTCTTCACTACAGCTCACGGCCCATCTGCCCGAAGCACTGCAAGGTGCC 1203

QY 1213 CGCACGCTCTTCAAAATTCTTCTTGGTTCGGCTACTGCAACAGCTCGTTGAACCCGGTC 1272

Db 1204 CATGGCCTCTTCCAGTTCTTCTTCTGATCGGCTACTGCAACAGCTCACTGAACCCCTGTT 1263

QY 1273 ATCTACACCATCTTCAACCAACGATTTCGCGCGCGCCTTCAAGAAGATCCTCTGTCTG 1328

Db 1264 ATCTACACCATCTTCAACCAACGACTTCCGCGCGTGCCTTCCGAGGATCCTGTGCGG 1319

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:31:11 ; Search time 95.1114 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174	12.9	3335	1 US-07-676-174A-1	Sequence 1, Appli
2	168	12.4	1335	2 US-08-985-090-3	Sequence 3, Appli
3	168	12.4	1335	3 US-09-165-543-3	Sequence 3, Appli
4	168	12.4	2689	2 US-08-985-090-1	Sequence 1, Appli
5	168	12.4	2689	3 US-09-165-543-1	Sequence 1, Appli
6	166.4	12.3	1335	3 US-09-167-354-6	Sequence 6, Appli
7	166.4	12.3	1335	4 US-09-642-855-6	Sequence 6, Appli
8	166.4	12.3	1335	4 US-09-642-514-6	Sequence 5, Appli
9	166.4	12.3	2699	3 US-09-167-354-5	Sequence 5, Appli
10	166.4	12.3	2699	4 US-09-642-855-5	Sequence 5, Appli
11	166.4	12.3	2699	4 US-09-642-514-5	Sequence 5, Appli
12	153	11.3	2428	3 US-08-475-742-15	Sequence 15, Appl
13	151.8	11.2	2140	1 US-08-334-698-1	Sequence 1, Appli
14	151.8	11.2	2140	1 US-08-228-932-1	Sequence 1, Appli
15	151.8	11.2	2140	1 US-08-468-939-1	Sequence 1, Appli
16	151.8	11.2	2140	2 US-08-406-855A-1	Sequence 1, Appli
17	151.8	11.2	2140	2 US-08-722-190-1	Sequence 1, Appli
18	151.8	11.2	2140	3 US-08-244-354-1	Sequence 1, Appli
19	151.8	11.2	2140	3 US-09-206-899-1	Sequence 1, Appli
20	151.8	11.2	2140	4 US-09-444-783-1	Sequence 1, Appli
21	151.8	11.2	2140	4 US-09-688-415-1	Sequence 1, Appli
22	151.8	11.2	2140	5 PCT-US95-04203-1	Sequence 1, Appli
23	151	11.2	3335	1 US-08-194-338-1	Sequence 1, Appli
24	150.6	11.2	1621	1 US-08-722-001-13	Sequence 13, Appl
25	150.4	11.1	1956	1 US-08-313-553-6	Sequence 6, Appli
26	150.4	11.1	1956	3 US-08-767-993-6	Sequence 6, Appli
27	150.2	11.1	1776	1 US-08-722-001-29	Sequence 29, Appl

28	147.2	10.9	1645	2 US-08-461-812-1	Sequence 1, Appli
29	142	10.5	1134	1 US-08-087-772A-14	Sequence 14, Appl
30	142	10.5	1227	1 US-07-916-901-1	Sequence 1, Appli
31	142	10.5	3683	4 US-08-450-962-1	Sequence 1, Appli
32	141	10.4	1610	1 US-08-056-051-5	Sequence 5, Appli
33	141	10.4	1610	1 US-07-928-611-21	Sequence 21, Appl
34	141	10.4	1610	2 US-08-487-811A-21	Sequence 21, Appl
35	141	10.4	1610	4 US-09-060-694-21	Sequence 21, Appl
36	141	10.4	1610	4 US-09-378-074-21	Sequence 21, Appl
37	141	10.4	1610	5 PCT-US93-07370-21	Sequence 21, Appl
38	140.8	10.4	1581	1 US-08-313-553-8	Sequence 8, Appli
39	140.8	10.4	1581	3 US-08-767-993-8	Sequence 8, Appli
40	140.4	10.4	1227	1 US-08-351-473B-7	Sequence 7, Appli
41	139.8	10.4	1338	3 US-09-165-543-6	Sequence 6, Appli
42	139.8	10.4	1690	2 US-08-461-812-3	Sequence 3, Appli
43	139.8	10.4	3244	3 US-09-165-543-4	Sequence 4, Appli
44	138.2	10.2	1601	1 US-08-722-001-7	Sequence 7, Appli
45	138.2	10.2	1997	1 US-08-722-001-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-07-676-174A-1
; Sequence 1, Application US/07676174A
; Patent No. 5344776
; GENERAL INFORMATION:
; APPLICANT: Vantor, J. Craig
; TITLE OF INVENTION: Octopamine receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,174A
; FILING DATE: 19910328
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)861-3000
; TELEFAX: (202)822-8944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3335 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 319..2121
; US-07-676-174A-1

Query Match 12.9%; Score 174; DB 1; Length 3335;
Best Local Similarity 56.2%; Pred. No. 2.8e-23;
Matches 352; Conservative 0; Mismatches 265; Indels 9; Gaps 1;

QY 128 TCATGCTGCTACCGTGTTCGGCAACGTGCTCGTCATCATCGCCGTTACGAGCCGCG 187
Db 674 TTATCGTGCTGACCATCATCGGGAAACATCCTCGGTGATTCTGAGTGTGTTCACTACAAGC 733

QY 837 GCCCGCGCCGGCGGG 852
Db 846 AGGCGCTGAGGCCGGG 861

RESULT 3
US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335

Query Match 12.4%; Score 168; DB 3; Length 1335;
Best Local Similarity 51.4%; Pred. No. 3e-22;
Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAGCGGACGGGCAACCGGAGCTGGAACGGGACCGAGGCGCGGGGG 62
Db 6 GCGCGCGCGCGGCGCGGCTTCTCGGCGAGCTGGACCGGCTGCTGGCGGCGAGCGCGGC 65

QY 63 CGGCGCGCGGCGCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCTGGCGG 122
Db 66 GCGGCGGCGGCGCGGCTTCTCGGCGAGCTGGACCGGCTGCTGGCGCGCTCATGSC 125

QY 123 CCTGCTCATGCTCATCCCGTGTTCGGCAACGTCGTCATCATCGCCGTTTCACGAG 182
Db 126 GCTGCTCATGTCGTCACGGTGTGTCGGCAACGCGTGTGTCATGCTCGCCTTCGTGGCCGA 185

QY 183 CCGCGCGCTCAAGGCGCCCCAAACCTCTTCCTGGTGTCTCTGGCTCGGCCGACATCCT 242
Db 186 CTCGAGCCTCCGACCCAGAACACITCTCTGCTCAACCTCGCCATCTCCGACTTCT 245

QY 243 GGTGGCCACGCTCGTCATCCCTTTCTCGCTGGCCAAACGAGGTATGGGCTACTGGTACTT 302

Db 246 CGTCGGCGCCTTCTGCATCCCACTGTATGTACCTACGTCTGACAGGCCGCTGGACCTT 305

QY 303 CGGCAAGGCTTGGTCGAGATCTACCTGGCGCTCGACGTGCTCTTCTGACGTGCTCCAT 362
Db 306 CGGCGGGGGCCTCTGCAAGCTGTGGCTGTGAGTGTGACTACCTGCTGTGACACTCCTCTGC 365

QY 363 CGTGCACCTGTGCGCATCAGCCTGGACCGCTACCGCTACTGGTCCATCACACAGGCCATCGAGTA 422
Db 366 CTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCTCGGTACCCGAGCGGTCTCATTA 425

QY 423 C---AACCTGAAGCGCACGCCGCGCGCATCAAGGCCATCATCATCACCGTGTGGGTCTAT 479
Db 426 CCGGGCCAGCAGGCTGACACGCGGGGCGAGTGTGCGGAAGATGCTGCTGGTGTGGGTGCT 485

QY 480 CTCGGCCGTCTCTCTTCCGCGCGCTCATCTCCATCGAGAAGAGGGCGGCGGCGG 539
Db 486 GGCCTTCTGTGTACGACCGCATCTCTGAGTGGGAGTACCTGTCCGGGGGCGAGCTC 545

QY 540 CCGCGACCGCGCGGCGCGCTGCGAGATCAACGACCCAGAAAGTGGTACGTCTCATCTCGTC 599
Db 546 CATCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCTCTCATCACGGC 605

QY 600 GTGCATCGGCTCCTTCTTCTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGGCGCATCTA 659
Db 606 TTCCACCTGGAGTTCTTACGCCCTTCTCAGCGTCACCTTCTTTAACTCAGCATCTA 665

QY 660 CCAGATCGCCAAAGCTCGCACCCGCGTGCACCCAGCCGCGGGTCCGGACGCCGTCGC 719
Db 666 CTTGAACATCCAGAGGCGCACCCGCTCCGGCTGGATGGGCTCGAGAGGCGAGCCGCGCC 725

QY 720 CGCGCCCGGGGCGACCGAGCGCAGGCCCAACCGTCTG---GGCCCGAGCGCAGCGC 776
Db 726 CGAGCCCCCTCCCGAGGCCAGCCCTCACCAACCCACCGCTGGCTGGTGGGCTGCTG 785

QY 777 GGGCCCGGGGCGCAGAGGCGGAAACCGCTGCCCCACCCAGCTCAACGCGCCCCCTGGCGA 836
Db 786 GCAGAAAGGGCACGCGGAGGCCATGCCGCTGCACAGGTATGGGTGGTGGGCGGCCGT 845

QY 837 GCCCGCGCGCGCGG 852
Db 846 AGGCGCTGAGGCCGGG 861

RESULT 4
US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030

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; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-08-985-090-1

Query Match 12.4%; Score 168; DB 2; Length 2689;
Best Local Similarity 51.4%; Pred. No. 3.2e-22;
Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAGCCGGACGCGGCAACGCGAGCTGGAACGGGACCGAGGCGCCGGGGG 62
Db 296 GCGCGCGCCCGCCGACGGCCGCTGAACGCTTCGGGGCGGTGGCGGCGAGCGCGGC 355
QY 63 CGGCGCCCGGGCCACCCCTTACTCCCTGCAGGTGACGTGCTCATCATCGCGGTGTC 122
Db 356 GCGGGCGGGGCGCGGGCTTCTCGGCAGCCTGGACCGCGGTGCTGGCGCGCTCATGC 415
QY 123 CCTGCTCATGCTGCACCGTGTTCGGCAACGTGCTGCTCATCATCGCGGTGTTCA 182
Db 416 GCTGCTCATGCTGGCCACGGTGTGGGCAACGGCTGGTTCATGCTCGCTTCGTGG 475
QY 183 CCGCGCGCTCAAGGGCCCCCAAAACCTCTTCTGGTGTCTCTGGCCTCGGCCGACAT 242
Db 476 CTCGAGCCTCCGCACCCAGAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTC 535
QY 243 GGTGGCCACGCTCGTATCCCTTTCTCGCTGGGCCAACGAGGTGATGGGTACTGTA 302
Db 536 CGTCGGCGCCTTCTGATCCCACTGTATGTACCTACGTGTGACAGCGCGTGGACCT 595
QY 303 CGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCT 362
Db 596 CGGCCGGGCGCTCTGCAAGCTGTGGCTGGTAGTGGAATACTGCTGTGCACCTCT 655
QY 363 CGTGACCTGTGCGCCATCAGCCTGGACCGTACTGGTCCATCACACAGGCCATCGA 422
Db 656 CTTCAACATCGTGTCTATCAGCTACGACCGCTCTCTGCGTCAACCGAGCGGTCT 715
QY 423 C---AACCTGAAGCGCAGCGCGCGCATCAAGCCATCATCATCACCGTGTGGTCA 479
Db 716 CCGGGCCACGAGGTGACACGCGGGCGGAGTGGGAAGATGCTGTGTGGTGTCT 775
QY 480 CTCGGCGGTATCTCTTCCCGCGCTCATCTCCATCGAAGAAGGGCGGCGCGCGG 539
Db 776 GGCCTTCTGTGTACGACACAGCCATCTTGAGCTGGGAGTACCTGTCCGGGGCAG 835
QY 540 CCGCAGCCCGCGAGCCGGCTGCGAGATCAACGACCAGAGTGGTACGTATCTCGTC 599
Db 836 CATCCCCGAGGGCCACTGTATGCCGAGTTCTTCTACAACTGGTACTTCTCTCAT 895
QY 600 GTGCATCGGCTCTTCTGCTCCCTGCTCATCATGATCCTGGTCTACGTGCGCATCT 659
Db 896 TTCCACCTTGAGTTCTTTACGCCCTTCTCTACGCTCACCTTCTTTAACCTCAG 955
QY 660 CCAGATCGCAAGCGTCGCACCCCGCTGCCACCCAGCCCGGGGTCCGACCGCGT 719
Db 956 CTTGAACATCCAGAGGCGCACCCGCTCCGCTGGATGGGCTCGAGAGGACGCGGCC 1015
QY 720 CGCGCCCGGGGGCACCGAGCGCAGGCCCAACGGTCTG--GGCCCCAGCGCAGCG 776
Db 1016 CGAGCCCCCTCCCGAGGCGCCAGCCCTCACCAACCCACCGCTGGCTGTGGGCT 1075
QY 777 GGGCCGGGGGGCGCAGAGCGCGAACCGCTGCCCCACCCAGCTCAACGGGCCCCCT 836
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Db 1076 GCAGAGGGGCACGGGAGGCCATGCCGCTGCACAGGTATGGGTGGTGAGGCGCGCT 1135
QY 837 GCCCGCGCCGCGCGG 852
Db 1136 AGCGCTGAGGCGCGG 1151

RESULT 5
US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-09-165-543-1
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Query Match 12.4%; Score 168; DB 3; Length 2689;
Best Local Similarity 51.4%; Pred. No. 3.2e-22;
Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAGCCGGACGCGGCAACGCGAGCTGGAACGGGACCGAGGCGCCGGGGG 62
Db 296 GCGCGCGCCCGCCGACGGCCGCTGAACGCTTCGGGGCGGTGGCGGCGAGCGCGGC 355
QY 63 CGGCGCCCGGGCCACCCCTTACTCCCTGCAGGTGACGTGCTCATCATCGCGGTGTC 122
Db 356 GCGGGCGGGGCGCGGCTTCTCGGCAGCCTGACCGCGGTGCTGGCGCGCTCATGGC 415
QY 123 CTTGCTCATGCTGCACCGTGTTCGGCAACGTGCTGCTCATCATCGCGGTGTTCA 182
Db 416 GCTGCTCATGCTGGCCACGGTGTGGGCAACGGCTGGTTCATGCTCGCTTCGTGG 475
QY 183 CCGCGCGCTCAAGGGCCCCCAAAACCTCTTCTGGTGTCTCTGGCCTCGGCCGACAT 242
Db 476 CTCGAGCCTCCGCACCCAGAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTC 535
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QY	243	GGTGGCCACGCTCGTCAATCCCTTTCTCGCTGGCCAAACGAGGTCAATGGGCTACTGGTACTT	302
Db	536	CGTCGGCGCCTTCTGCATCCCACTGTATGTACCCCTACGTGTGACAGGCCGCTGGACCTT	595
QY	303	CGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGCTCTTCTGACAGTCGTCCAT	362
Db	596	CGGCCGGGGCCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACCTCCTCTGTC	655
QY	363	CGTGCACCTGTGGGCCATCAGCCTGGACCGCTACTGTGTCATCAACAGGCCATCGAGTA	422
Db	656	CTTCAACATCGTGCTCATCAGCTACGACCGCTTCTGTGCGTCAACCGAGCGTCTCATA	715
QY	423	C---AACCTGAAGCGCACGGCGCGCCGCATCAAGGCCATCATCACCGTGTGGGTGCT	479
Db	716	CCGGCCCAAGAGGTGACACGGCGGGCGGAGTGCGGAAGATGCTGTGGTGTGGGTGCT	775
QY	480	CTCGGCCGTCACTCTTCCTCCGCGCGCTCATCTCCATCGAGAAGAGGGCGGCGGCGG	539
Db	776	GGCCTTCTCTGTGTACGACACAGCCATCCTGAGCTGGAGTACCTGTCCGGGGGACGCTC	835
QY	540	CCCGCAGCCGGCCGAGCCCGCTGCGAGATCAACGACAGCAAGTGGTACGTCACTCTGTC	599
Db	836	CATCCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACGTGGTACTTCTCTCATCAGGC	895
QY	600	GTGCATCGGCTCCTTCTTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGCGCATCTA	659
Db	896	TTCCACCTGGAGTCTTTACGCCCTTCTCAGCGTCACTTCTTTAACCTCAGCATCTA	955
QY	660	CCAGATCGCCAAGCTCGCACCCGCGTGCCACCCAGCCGCGGGGTCCGGACGCCGTGCG	719
Db	956	CCTGAACATCCAGAGGCGACCCGCCCTCCGGCTGGATGGGGCTCGAGAGGCAGCCGGCCC	1015
QY	720	CGCGCCGCGGGGGACCGAGCGCAGGGCCCAACGGTCTG---GGCCCCGAGCGCAGCGC	776
Db	1016	CGAGCCCCCTCCCCGAGGCCAGCCCTCACCAACCCCCACCGCTGGCTGTGGGGCTGCTG	1075
QY	777	GGGCCCGGGGGCGCAGGCCCGAACCGCTGCCCAACCCAGCTCAACGGCGCCCCCTGGCGA	836
Db	1076	GCAGAAGGGGCACGGGGAGGCCATGCCGCTGCACAGGTATGGGTGGGTGAGCGGCCGT	1135
QY	837	GCCCGCGCCGCCGGG	852
Db	1136	AGGCGCTGAGGCCGGG	1151

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RESULT 6
US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JWM
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-6

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QY	3	GGGCTCCCTGCAGCCGGACCGGGCAACCGGAGCTGGAAACGGGACCGAGGCGCCGGGGGG	62
Db	6	GGCGCGCGCCGACGGGCGCTGAACGCTTCGGGGGCGCTGGCGGGCGATGCGGCGGC	65
QY	63	CGGCGCCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCTTGGCCGG	122
Db	66	GGCGGCGGGCGCGCGCTTCTCGSAGCCTGGACCGCGGTGCTGGCCGCGCTCATGGC	125
QY	123	CCTGCTCATGTGCTCACCGTGTTCGGCAACGTGCTCGTCATCATCGCCGTGTTCAAGAG	182
Db	126	GCTGCTCATCGTGGCCACGGTGTGGCAACGCGTGGTCATGCTCGCCTTCGTGGCCGA	185
QY	183	CCGCGCGCTCAAGGCGCCCCAAACCTCTTCTCGGTGTCTTGGCCTCGGCCGACATCCT	242
Db	186	CTCGAGCCTCCGCACCCAGAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCCT	245
QY	243	GGTGGCCACGCTGTCATCCCTTTCTCGCTGGCCAAACGAGGTGATGGGCTACTGGTACTT	302
Db	246	CGTCCGGCGCTTCTGCATCCCACTGTATGCCCTACGTGCTGACAGGCGCGTGGACCTT	305
QY	303	CGGCAAGGCTTGGTGCAGATCTACCTGGCGCTCGACGTGCTTCTGCAACGTGTCAT	362
Db	306	CGGCCGGGCTCTGCAAGCTGTGGTGGTAGTGAGTACCTGCTGTGCACCTCCTCTGC	365
QY	363	CGTGACCTGTGCGCCATCAGCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTA	422
Db	366	CTTCAACATCTGTCTCATCAGCTACGACCGCTTCTCTGTCGGTCAACCGAGCGGTCTCAT	425
QY	423	C---AACCTGAAGCGCACGCCGCGCGCATCAAGGCCATCATCATCACCGTGTGGGTGAT	479
Db	426	CCGGGCCACAGCAGGTGACACGCGCGGGCAGTGCGGAAGATGCTGCTGGTGTGGGTGCT	485
QY	480	CTCGGCGTCATCTCTTCCCGCGCTCATCTCCATCGAGAAAGGCGCGCGGCGCGG	539
Db	486	GGCCTTCTGCTGTACGGACCGCATCCTGAGCTGGAGTACCTGTCCGGGSGAGCTC	545
QY	540	CCCGCAGCCGCGCAGCCGCGTGCAGAGATCAACGACAGAAAGTGGTACGTCTATCTCGTC	599
Db	546	CATCCCCGAGGGCCACTGCTATGCGGAGTTCTTCTACAACTGGTACTTCTCTCATCACGGC	605
QY	600	GTGCATCGGCTCTTCTTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGGCATCTA	659
Db	606	TTCCACCTTGGAGTTCTTTACGCCCTTCTCAGCGTCACTTCTTTAACCTCAGCATCTA	665
QY	660	CCAGATCGCCAAAGCGTCGCACCGCGGTGCCACCCAGCGCGCGGGTCCGGACGCCGTGCG	719
Db	666	CCTGAACATCCAGAGCGCACCGCGCTCCGGTGGATGGGGCTCGAGAGGACCGGCCCC	725
QY	720	CGCGCGCGCGGGGACCGAGCGCAGGCCCAACCGTGTG---GGCCCCGAGCGCAGCGC	776
Db	726	CGAGCCCCCTCCGAGGCCCCAGCCTCACCACCCCCAGCCTGGCTGCTGGGGCTGCTG	785
QY	777	GGGCCCCGGGGCGCAGAGGCCGAACCGTGCCCAACCCAGCTCAACGGCGCCCCCTGGCGA	836
Db	786	GCAGAAGGGGCACGGGAGGCCATGCCGCTGCACAGGTATGGGGTGGGTGAGCGCGCCGT	845
QY	837	GCCCGCGCGCGCGCGG	852
Db	846	AGCGCTGAGGCCGGG	861

RESULT 7
 US-09-642-855-6
 ; Sequence 6, Application US/09642855
 ; Patent No. 6413743
 ; GENERAL INFORMATION:
 ; APPLICANT: Lovenberg, Timothy
 ; APPLICANT: Erlander, Mark
 ; APPLICANT: Pyati, Jayashree
 ; APPLICANT: Huvar, Arne
 ; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
 ; SUBTYPE

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; FILE REFERENCE: JWW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-855-6

Query Match      12.3%; Score 166.4; DB 4; Length 1335;
Best Local Similarity 51.3%; Pred. No. 5.8e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAGCCGGACGCGGCAACGCGAGCTGGAACGGGACCGAGGCGCGGGGG 62
Db 6 GCGCGCGCGCCCGACGGCCGCTGAACGCTTCGGGGCGCTGGCGGCGATGCGGCGGC 65
QY 63 CGGCGCCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCCGG 122
Db 66 GCGCGCGGGCGCGCGGCTTCTCGGCAGCTGGACCGGCTGCTGGCCGCGCTCATGGC 125
QY 123 CCTGCTCATGTCTACCGTGTTCGGCAACGCTGCTCGTCATCATCGCCGTGTTACAGG 182
Db 126 GCTGCTCATCGTGGCACGGTGTCTGGCAACGCGCTGGTCATGCTCGCCTTCGTGGCCGA 185
QY 183 CCGCGCGCTCAAGGGCGCCCAAAACCTTCTCTGGTGTCTCTGGCTCGGCCGACATCCT 242
Db 186 CTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCCT 245
QY 243 GGTGGCCACGCTCGTCACTCCCTTCTCGCTGGCCAAACGAGGTGATGGGCTACTGTA 302
Db 246 CGTCGGCGCCTTCTGCATCCCACTGTATGTACCCCTACGCTGACAGGCGCTGGACCTT 305
QY 303 CGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCTGTCAT 362
Db 306 CGGCGGGGCGCTCTGCAAGCTGTGGCTGGTAGTGACTACCTGCTGTGCACCTCCTCTGC 365
QY 363 CGTGACCTGTGCGGCATCAGCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTA 422
Db 366 CTTCAACATCGTCTCATAGTACGACCGCTTCTGTCGGTACCCCGAGCGGTCTCATA 425
QY 423 C---AACCTGAAGCGCACGCGCGCGGCATCAAGGCCATCATCATCACCGTGGGTGCAT 479
Db 426 CCGGGCCAGCAGGGTGACACGCGCGGGGAGTGCGGAAGATGCTGCTGGTGGGTGCT 485
QY 480 CTCGGCCGTCACTCCTTCCGCGCGCTCATCTCCATCGAGAAGAGGGCGGCGCGCGG 539
Db 486 GGCCTTCTCTGTACGGACCAAGCCATCCTGAGCTGGGAGTACCTGTCCGGGGGAGTCTC 545
QY 540 CCGCAGCCGCGCGGCTGCGAGATCAACGACCAAGAGTGGTACGTCACTCTCGTC 599
Db 546 CATCCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACCTGGTACTTCTCATCACGGC 605
QY 600 GTGCATCGGCTCCTTCTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGGCGCATCTA 659
Db 606 TTCCACCTGGAGTTCTTTACGCCCTTCTTCAGCGTCACTTCTTTAACCTCAGCATCTA 665
QY 660 CCAGATCGCCAAAGCTCGACCCCGCTGCCACCCAGCCCGGGTCCGGAGCGCGCTCGC 719
Db 666 CTTGAACATCCAGAGGGCGACCCGCTCCGGCTGGATGGGCTCGAGAGGCGAGCGGCCCC 725
QY 720 CGCGCCCGCGGGGGCACCGAGCGCAGGCCCAACCGTCTG---GGCCCCGAGCGCAGCGC 776
Db 726 CGAGCCCGCTCCCGAGGCCAGGCTCACCAACCCACCGCCTGGCTGGCTGGGCTGCTG 785
QY 777 GGGCCCGGGGGCGCAGAGGCCGAACCGCTGCCCAACCCAGCTCAACGCGGCCCTGGCGGA 836

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Db 786 GCAGAAAGGGCACGGGAGGCCATGCCGCTGCACAGGTATGGGGTGGGTGAGGCGGCCGT 845
QY 837 GCCCGCGCGCGCGCGGG 852
Db 846 AGCGCTGAGCGCGGG 861

RESULT 8
US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: ORTI290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6

Query Match      12.3%; Score 166.4; DB 4; Length 1335;
Best Local Similarity 51.3%; Pred. No. 5.8e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAGCCGGACGCGGCAACGCGAGCTGGAACGGGACCGAGGCGCGGGGG 62
Db 6 GCGCGCGCGCCCGACGGCCGCTGAACGCTTCGGGGCGCTGGCGGCGATGCGGCGGC 65
QY 63 CGGCGCCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCCGG 122
Db 66 GCGCGCGGGCGCGCGGCTTCTCGGCAGCTGGACCGGCTGCTGGCCGCGCTCATGGC 125
QY 123 CCTGCTCATGTCTACCGTGTTCGGCAACGCTGCTCGTCATCATCGCCGTGTTACAGG 182
Db 126 GCTGCTCATCGTGGCCACGGTGTCTGGCAACGCGCTGGTCATGCTCGCCTTCGTGGCCGA 185
QY 183 CCGCGCGCTCAAGGGCGCCCAAAACCTTCTCTGGTGTCTCTGGCTCGGCCGACATCCT 242
Db 186 CTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCCT 245
QY 243 GGTGGCCACGCTCGTCACTCCCTTCTCGCTGGCCAAACGAGGTGATGGGCTACTGTA 302
Db 246 CGTCGGCGCCTTCTGCATCCCACTGTATGTACCCCTACGCTGACAGGCGCTGGACCTT 305
QY 303 CGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCTGTCAT 362
Db 306 CGGCGGGGCGCTCTGCAAGCTGTGGCTGGTAGTGACTACCTGCTGTGCACCTCCTCTGC 365
QY 363 CGTGACCTGTGCGGCATCAGCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTA 422
Db 366 CTTCAACATCGTGTCTCATAGTACGACCGCTTCTGTCGGTACCCCGAGCGGTCTCATA 425
QY 423 C---AACCTGAAGCGCACGCGCGCGGCATCAAGGCCATCATCATCACCGTGGGTGCAT 479
Db 426 CCGGGCCAGCAGGGTGACACGCGCGGGGAGTGCGGAAGATGCTGCTGGTGGGTGCT 485
QY 480 CTCGGCCGTCACTCCTTCCGCGCGCTCATCTCCATCGAGAAGAGGGCGGCGCGCGG 539
Db 486 GGCCTTCTCTGTACGGACCAAGCCATCCTGAGCTGGGAGTACCTGTCCGGGGGAGTCTC 545
QY 540 CCGCAGCCGCGCGGCTGCGAGATCAACGACCAAGAGTGGTACGTCACTCTCGTC 599
Db 546 CATCCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACCTGGTACTTCTCATCACGGC 605
QY 600 GTGCATCGGCTCCTTCTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTGGCGCATCTA 659
Db 606 TTCCACCTGGAGTTCTTTACGCCCTTCTTCAGCGTCACTTCTTTAACCTCAGCATCTA 665
QY 660 CCAGATCGCCAAAGCTCGACCCCGCTGCCACCCAGCCCGGGTCCGGAGCGCGCTCGC 719
Db 666 CTTGAACATCCAGAGGGCGACCCGCTCCGGCTGGATGGGCTCGAGAGGCGAGCGGCCCC 725
QY 720 CGCGCCCGCGGGGGCACCGAGCGCAGGCCCAACCGTCTG---GGCCCCGAGCGCAGCGC 776
Db 726 CGAGCCCGCTCCCGAGGCCAGGCTCACCAACCCACCGCCTGGCTGGCTGGGCTGCTG 785
QY 777 GGGCCCGGGGGCGCAGAGGCCGAACCGCTGCCCAACCCAGCTCAACGCGGCCCTGGCGGA 836

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Db 1144 AGGCGTGAAGCGGG 1159

RESULT 12

US-08-475-742-15

; Sequence 15, Application US/08475742

; Patent No. 6121015

; GENERAL INFORMATION:

; APPLICANT: O'Malley, Karen L

; APPLICANT: Todd, Richard D

; TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor

; FILE REFERENCE: WU 102 CON DIV

; CURRENT APPLICATION NUMBER: US/08/475,742

; CURRENT FILING DATE: 1995-06-07

; EARLIER APPLICATION NUMBER: US 08/261,293

; EARLIER FILING DATE: 1994-06-16

; EARLIER APPLICATION NUMBER: US 08/014,013

; EARLIER FILING DATE: 1993-01-28

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 2428

; TYPE: DNA

; ORGANISM: cdna

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(2428)

; OTHER INFORMATION: Rat d2 receptor sequence

; PUBLICATION INFORMATION:

; TITLE: Cloning and expression of a rat D2 dopamine receptor

; TITLE: cdna.

; JOURNAL: Nature

; VOLUME: 336

; PAGES: 783-787

; DATE: 1988

US-08-475-742-15

Query Match 11.3%; Score 153; DB 3; Length 2428;

Best Local Similarity 48.8%; Pred. No. 1.6e-19;

Matches 594; Conservative 0; Mismatches 605; Indels 18; Gaps 6;

QY 115 CTGGCGGCGCTCATGCTGCTCACCGTGTTCGGCAACGTGCTCGTCATCATCGCCGCTG 174

Db 142 CTGCTCACCTCCTCATCTTATCATCGTCTTTGGCAATGTGCTGGTGCATGGCTGTA 201

QY 175 TTCAGAGCGCGCGCTCAAGGCGGCCCAAAACCTTCTCCTGGTGTCTCTGGCCTCGGCC 234

Db 202 TCCGAGAGAAGGCTTTGCAGACCACCACCACTACTTGATAGTCAGCCTTGCTGTGGCT 261

QY 235 GACATCCTGGTGGCCACGCTCGTCATCCCTTTCTCGTGGCCAAACGAGGTATGGGCTAC 294

Db 262 GATCTTCTGGTGGCCACACTGGTAATGCCGTGGGTTGTCTACCTGGAGGTGGTGGTGAG 321

QY 295 TGGTACTTCGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCAAG 354

Db 322 TGGAAATTCAGCAGGATTCACTGTGACATCTTTGTCACTCTGGATGTATGATGTGCACA 381

QY 355 TCGTCCATCGTGCCCATCATGAGCGCTGAGCGCTACTGGTCCATCATCACAGGCC 414

Db 382 GCAAGCATCTGAACCTGTGTGCCATCAGCATTCAGAGGTACACAGCTGTGGCAATGCC 441

QY 415 ATCGAGTACAAC---CTGAAGCGCACGCCGCGCATCAAGGCCATCATCACCGTG 471

Db 442 ATGCTGTATAACACACGCTACAGCTCCAAGCGCCGAGTTACTGTCTATGATGCCATTGTC 501

QY 472 TGGGTCACTCTGGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGGGGGC 531

Db 502 TGGTCTCTCTTACCATCTCTCTGCCCACTGCTCTCGGACTCAACATACAGACCAG 561

QY 532 GCGGCGGCGCGCAGCGCGCGAGCGCGCTGGAGATCAACGACCAAGTGGTACGTC 591

Db 562 AATGAGTG---TATCATTGCCAAACCTGCCCTTGTGGTCTACTCCTCCATTGTCTCATTC 618

QY 592 ATCTCGTGTGATCGGCTCCTTCTTCGCTCCCTGCCTCATCATGATCCTGGTCTACGTG 651

Db 619 TACGTGCCCTTCATCGTCACTCTGCTGCTGTATATCAAAATCTACATCGTCTCCGGAAG 678

QY 652 CGCATCTACAGATCGCCAAGCGTGCACCCGCGTGCACCCAGCGCGGGTCCGGAC 711

Db 679 CGCCGGAAGCGGTTCAACACCAAGCGCAGCAGTCGAGCTTTCAG-AGCCAAACCTGAAGAC 737

QY 712 GCCGTGCGCGCGCGCGGGGCGACAGAGCGCAGGCCCCAACGGTCTTGGGCCCCGAGCGC 771

Db 738 ACCACTCAAGGGCAAC-----TGTAACCCACCTGAGGACATGAAGAACTCTGCACCGTTATC 792

QY 772 AGCGCGGCGCGGGGCGCAGAGGCGGAACCGCTGCCACCCAGCTCAACGGGCGCCCT 831

Db 793 ATGAAGTCTAATGGGAGTTTCCAGTGAACAGCGGAGAAATGGATGCTGCCCGCGGAGCT 852

QY 832 GCGAGCGCGCGCGCGCGCGCGCGCGCGCAGCAGCGCGCTGGACCTG---GAGGAGAGC 888

Db 853 CAGGAGCTGGAATGGAGATGCTGTCAAGCACCGCCCCCAGAGAGGAGACCGGTATAGC 912

QY 889 TCGTCTTCCGACCGCGGAGCGGCTCCAGGGCCCCGCGAGACCCGAGCGCGGTCCCCGG 948

Db 913 CCCATCCCTCCAGTCAACCACAGTCACTCTCCCTGATCATCCACACCGGCTACAT 972

QY 949 GGCAAGGCAAGGCCGAGCGAGCGAGGTGAAGCCGGCGAGAGCTTCCGCGCGCGGG 1008

Db 973 AGCAACCTGACAGTCTTGCCAAACAGAGAGAAGATGGGCAGCCCAAGATTGTCAATCCC 1032

QY 1009 CCGGGGCGACGGGATCGGGACGCGCGCTGCAGGGCCGGGAGGAGCGCGTTCGGGCT 1068

Db 1033 AGGATTGCCAAGTTCTTTGAGATCCAGACCATGCCCAATGSCAAAACCCGGACCTCCCTT 1092

QY 1069 GCCAAGCGCTCGCGCTGGCGCGGGCGCGCAGAACCCGCGAGAAAGCGCTTCACGTTGCTG 1128

Db 1093 AAGACGATGAGCCGCGAGAAAGCTTCCCAGCAGAGAGAGAAAGCCACTCAGATGCTT 1152

QY 1129 GCGTGTGTCATCGGAGTGTTCGTGGTGTGCTGGTTCCTTCTTCAACATCTTCTTCTGCTG 1188

Db 1153 GCCATTGTTCTCGGTGTGTTTCATCATCTGTGGTGGCTGCCCTTCTTTCATCAGCACATCCTG 1212

QY 1189 ACGGCGCTCGG---GTGCTCCGTGCCACGACGCTCTTCAAAATCTTCTTCTGCTGCGC 1245

Db 1213 AATATACACTGTGATTGCAACATCCCACAGTCCTCTACAGCGCTTTCACATGGTGGGC 1272

QY 1246 TACTGCAACAGCTCGTTGAACCGGTCATCTACACCATCTTCAACACGATTTCCGCGCGC 1305

Db 1273 TATGTCAACAGTGCCGTCAACCCCATCATCTACACCACTTCAACATCGAGTTCCGCAAG 1332

QY 1306 GCCTTCAAGAAGATCCT 1322

Db 1333 GCCTTCATGAAGATCTT 1349

RESULT 13

US-08-334-698-1

; Sequence 1, Application US/08334698

; Patent No. 5556753

; GENERAL INFORMATION:

; APPLICANT: Jonathan A. Bard et al.

; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic

; TITLE OF INVENTION: Receptors and Uses Thereof

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: COOPER & DUNHAM

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,698
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/952,798
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 376901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1893
; OTHER INFORMATION:
;
; PS-08-334-698-1

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Query Match	11.2%;	Score 151.8;	DB 1;	Length 2140;
Best Local Similarity	51.9%;	Pred. No. 2.6e-19;		
Matches 432: Conservative		0; Mismatches 377;	Indels 24;	Gaps 3;

QY	18	GGACGCGGCAACGCGAGCTGGAAACGGGACCGAGGCGCGGGGGCGCGCGCGGGCCAC	77
Db	387	GGAGCCGGGAGCGCGGCGCGGGCGCGAGCTGAATGGCACGGCGGCGCTCGGGGACT	446
QY	78	CCCTTACTCCCTGACAGGTGACGCTGACGCTGGTGTGCTGGCCGGCCCTGCTCATCTGCT	137
Db	447	GGTGTGAGCGCGCAGGGCGTGGGCGTGGGCGTCTTCCTGGCAGCC---TTCATCCTTAT	503
QY	138	CACCGTGTTCGGCAACGTGCTCGTCATCATCGCCGTGTTACAGAGCCGCGGCTCAAGGC	197
Db	504	GGCCGTGGCAGGTAACCTGCTTGTTCATCCTCTCAGTGGCTGCAACCGCCACCTGCAGAC	563
QY	198	GCCCCAAACCTCTTCTGGTGTCTCTGGCCTCGGCCGACATCCTGGTGGCCACGCTCGT	257
Db	564	CGTACCAACTATTTCATCGTGAACTGGCCGTGGCCGACCTGCTGTGAGCGCCACCGT	623
QY	258	CATCCCTTTCTCGCTGGCCAACGAGGTGATGGGCTACTGGTACTTCGGCAAGCCTTGGTG	317
Db	624	ACTGCCCTTCTCGGCCACCATGGAGTTCTGGGCTTCTGGGCTTTGGCCGCGCTTCTG	683
QY	318	CGAGATCTACCTGGCGCTCGACGTGCTCTTCTGACAGCTGTCCATCTGTGCACCTGTGCGC	377
Db	684	CGACGTATGGCGCGCGTGGACGTGTGTGCTGCACGGCCTCCATCCTCAGCCTCTGCAC	743
QY	378	CATCAGCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTACAACCTGAAGCGCAC	437
Db	744	CATCTCCGTGGACCGGTACGTGGCGGTGCGCCACTCACTCAAGTACCCAGCCATCATGAC	803
QY	438	GCCGCGCGCATCAAGGCCATCATCATCACCGTGTGGGTGATCTCGGCCGTCACTTCCTT	497
Db	804	CGAGCGCAAGGCGCGCCATCCTTGGCCCTGCTCTGGGTCTAGCCCTGGTGGTGTCCGT	863
QY	498	CCCGCGCTCATCTCCATCGAGAAAGAGGCGGGCGGGCGCCGAGCCCGCGGAGCC	557
Db	864	AGGGCCCCCT-----GCTGGGCTGGAAGGAGGCCCGTGCCTTACGAGCG	908
QY	558	GCGCTGCGAGATCAACGACGAGAGTGGTACGTATCTCGTCTGCATCGGCTCCTCTT	617

Db	909	CTTCTGCGGTATCACCGAGGAGCGGCTACGCTGCTTCTCCTCCGTGTGCTCCTTCTA	968
QY	618	CGCTCCCTGCCTCATCATGATCCTGGTCTACGTGCGCATCTACCAAGATCGC-----CAA	671
Db	969	CCTGCCCATGGCGGTTCATCGTGGTCATGTACTGCCGCGTGTACGTGGTCGCGCGCAGCAC	1028
QY	672	CGTTCGACCCGCGTGCACCCAGCCGCGGGGTCCGGACGCCGTGCGCGCGCCGCCGGG	731
Db	1029	CACGGCAGCCTCGAGGCAGGCGTCAAGCGCGAGCGAGGCAAGGCCCTCCAGAGTGGTGCT	1088
QY	732	GGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCGCAGCGCGGCCCCGGGGGGCGC	791
Db	1089	GCGCATCCACTGTTCGGCGCGGCCACCGGGCGCCGACGGGGCGCACCGGCATGCGCAGCGC	1148
QY	792	AGAGGCCGAACCGGTGCCCAACCCAGTCAACGGGCGCCCTGGCGAGCCCCGCGC	844
Db	1149	CAAGGGCCACACCTTCCGAGCTCGCTCTCCGTGGCCCTGCTCAAGTTCTCC	1201

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RESULT 14
US-08-228-932-1
; Sequence 1, Application US/08228932
; Patent No. 5578611
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
; APPLICANT: Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
; TITLE OF INVENTION: PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,932
; FILING DATE: 13-APR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1893
; OTHER INFORMATION:
;
US-08-228-932-1

```

Query Match	11.2%;	Score 151.8;	DB 1;	Length 2140;
Best Local Similarity	51.9%;	Pred. No. 2.6e-19;		
Matches 432: Conservative	0;	Mismatches 377;	Indels 24;	Gaps 3;

Db	909	CTTCTGCGGTATCACCGAGGAGGGGGCTACGCTGTCTTCTCCTCCGTGTGCTCTCTA	968
Qy	618	CGCTCCCTGCCTCATCATGATCCTGGTCTACGTGGCATCTACCAGATCGC-----CAA	671
Db	969	CCTGCCCCATGGCGGTCACTCGTGGTCAATGCTGCCGCGGTGTACGTGGTGGCGCGCAGCAC	1028
Qy	672	GCGTGCACCCCGGTGTCACCCAGCCGCCGGGTCCGACGCCCTCGCCGCGCCGCCGGG	731
Db	1029	CACGCGCAGCCTCGAGGAGGCGTCAAGCGCGAGCGAGGCAAGGCCCTCCGAGTGGTGCT	1088
Qy	732	GGGCACCGAGCGCGCCCAACGGTCTGGGGCCCCGACGCGCAGCGGGGCCCGGGGGCGC	791
Db	1089	GCGCATCCACTGTGCGGGCGCGGCCACGGGGCGCCGACGGGGCGGCACGGCATGCCAGCGC	1148
Qy	792	AGAGGCCGAACCGCTGCCACCCAGCTCAACGGGGCCCCCTGGCGAGCCCGCGC	844
Db	1149	CAAGGGCCACACCTTCCGAGACTCGCTCTCCGTGGCGCTGCTCAAGTTCTCC	1201

Search completed: March 11, 2003, 07:41:17
Job time : 108.111 secs